

IntellicGenetics

FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file seq2-seq1.res made by jdelaval on Sun 9 Feb 103 17:37:45-PST.

Query sequence being compared:	US-09-935-124A-2 (1-392)
Number of sequences searched:	6
Number of scores above cutoff:	6

Results of the initial comparison of US-09-935-124A-2 (1-392) with:
File : US09935124A.seq

STDEV	SCORE	
1	174	S
2	348	E
	392	R
	261	O
	218	F
	131	C
	87	B
	44	N
	0	U
		M
		B
		E
		R
		K
		O
		F
		S
		E
		Q
		U
		E
		N
		C
		B
		S

Sequence Name	Description	Length	Score	Score	Sig.	Frame
1.	US-09-935-124A-1 Sequence 1, Application U	473	392	392	2.04	3

Sequence Name	Description	Length	Int.	Opt.	Sig.	Frame
2. US-09-935-14A-1 Sequence 1,	Application U	472	14	24	-0.37	6
3. US-09-935-14A-1 Sequence 1,	Application U	472	8	72	-0.41	5
4. US-09-935-14A-1 Sequence 1,	Application U	473	37	37	-0.42	2
5. US-09-935-14A-1 Sequence 1,	Application U	473	6	28	-0.42	4
6. US-09-935-14A-1 Sequence 1,	Application U	474	6	49	-0.42	1
<hr/>						
1. US-09-935-14A-2 (1-392)	Sequence 1, Application US/0993512A					
US-09-935-14A-1 Sequence 1,	Application US/0993512A					

Sequence 1, Application US/09935124A
GENERAL INFORMATION:
APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Atchison, Robert
APPLICANT: Bogenberger, Jakob
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-000210us
CURRENT APPLICATION NUMBER: US/09/935,124A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/284,760
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 1422
TYPE: DNA
ORGANISM: Homo sapiens

Initial Score =	392	Optimized Score =	392	Significance =	2.00e-06
Residue Identity =	100%	Matches =	392	Mismatches =	0
Gaps =	0	Conservative Substitutions			
Translation Frame=	3				

QSPKSYSTAGRRBVIKEGSSFLSPFPGSRARRALGLRQVPEVHGCGWVEAATTTOPASSGRAPHPGR
400 410 420 430 440 450 460
AAAAGL
470

4. US-09-935-124A-2 (1-392)
US-09-935-124A-1 Sequence 1, Application US/09935124A

Sequence 1, Application US/09935124A
GENERAL INFORMATION:

APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Atchison, Robert
APPLICANT: Bogenberger, Jakob
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-000210us
CURRENT APPLICATION NUMBER: US/09/935,124A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/284,760
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 1422
TYPE: DNA

ORGANISM: Homo sapiens

Initial Score = 6 Optimized Score = 37 Significance = -0.42
Residue Identity = 17% Matches = 47 Mismatches = 191
Gaps = 38 Conservative Substitutions = 0
Translation Frame = 2

MDLFDLPEPERSPPAPAGKGAOKGPLLFDLPPASSTDSGSGGPLLFDLPPASGDSGLATISQWVKT
10 20 30 40 50 60 70
80 90 100 110 120 130 140
EGGAKRKTSEBKNGSEBELVEKKVCKASVIFGLKGYAERKGEREMODAHVILNDITEBCRPSSLITR
150 160 170 180 190 200 210
VSFAVFDHGIGIRASKFAQNLHQLIRKFKPGDVISVEKTVKCLDTPFKHTDEEFLKQASSQKPAWKDG
220 230 240 250 260 270 280
PPARVERP-RCSRAECLSLRPPPSLRHGPLRGPGAGALAAPGCRERSSERTPALXXPPSGQGYXLRING
290 300 310 320 330 340 350
10 20 30 40 50 60 70
STA-----TCVLAVNITLIYIANLGDSPALICRYNESQKHALSLSEKHPTOYEERMRIQKAGNVADGV
360 370 380 390 400 410 420
TFPFXSPTRKXMRFRFSCHINIPDGDKRER-----SEKXILRGEE--WQRAKGESLXSL
80 90 100 110 120 130 140
290 300 310 320 330 340 350
LGLYLEVSRNIGDQYKRCGVTSPDIRRCOLTPNDRFILLACDGLFKVTPPEAVNFI--SCLF-----DE
360 370 380 390 400 410 420
FGGLSEGLCGAEGEGDAGCPRPERRHRCVXAPIVPHYSGTFCCCFXMTWRNSLKTCTETASRLNQ
140 150 160 170 180 190 200
350 360 370 380 390 400 410 420
KIOTREGKSAADARYE-----AACRLNKAIVGSGADNVTV--MVRRIQH
210 220 230 240 250 260 270
KLSXRKCNQCRNREEMPFHFOAYXXRVXTSFOPEACLERWVHCIVCSQKROHSLYCPPRXSGNLVSLX
280 290 300 310 320 330 340 350
XGESKTSIKLPPQARXSNVXRADEDETEGWRKSGWACFGARAGVTLLHMGRAVOALRCHLCARHQTLLPADPQ
360 370 380 390 400 410 420
XQVHFWGLXWALQGLYPRSRRELHLVLSRGKXDPDGRFEVRRRRLRESLQQAQCGAAGLGRQRHCGGA

DRLRGARPGAMVLTXXKHFVCHIVCYVSGCTPPMVNKGSPFSEYKKK
430 440 450 460 470

5. US-09-935-124A-2 (1-392)
US-09-935-124A-1 Sequence 1, Application US/09935124A

Sequence 1, Application US/09935124A
GENERAL INFORMATION:

APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Atchison, Robert
APPLICANT: Bogenberger, Jakob
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-000210us
CURRENT APPLICATION NUMBER: US/09/935,124A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/284,760
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 1
LENGTH: 1422
TYPE: DNA

ORGANISM: Homo sapiens

Initial Score = 6 Optimized Score = 28 Significance = -0.42
Residue Identity = 18% Matches = 39 Mismatches = 131
Gaps = 42 Conservative Substitutions = 0
Translation Frame = 4

MDLFDLPEPERSPPAPAGKGAOKGPLLFDLPPASSTDSGSGGPLLFDLPPASGDSGLATISQWVKT
10 20 30 40 50 60 70
80 90 100 110 120 130 140
EGGAKRKTSEBKNGSEBELVEKKVCKASVIFGLKGYAERKGEREMODAHVILNDITEBCRPSSLITR
150 160 170 180 190 200 210
VSFAVFDHGIGIRASKFAQNLHQLIRKFKPGDVISVEKTVKCLDTPFKHTDEEFLKQASSQKPAWKDG
220 230 240 250 260 270 280
STATCVLAVNITLIYIANLGDSPALICRYNESQKHALSLSEKHPTOYEERMRIQKAGNVADGVLCVL
290 300 310 320 330 340 350
FTTNGV---DQVTKHTWCTHTKCTFKFYNTWRAGRAPPLSLASAPPSQRCRPSAPAPPCWACGCLL---
360 370 380 390 400 410 420
10 20 30 40 50 60 70
EVSISIDQYKRCGVTSPDIRRCOLTPNDR-----FILLACDGLFKVTPPEAVNFI--SCLF-----DE
360 370 380 390 400 410 420
---RS---GRRLR---TSLP--GSGSFHPRDKTXSSRLLGKRPRAHHPYKXTCHWGSAGSYCKRAQKX
80 90 100 110 120 130 140
360 370 380 390 400 410 420
GKSNADRYEACNRLLA-----NKAVORGSA---DNVTVMVVRRIQH
140 150 160 170 180 190 200 210
HRSACTARPMWSTYPLARKAHHPYRFLQPSVSSSLHTLDELALCXGLRLHVFDSPHYNDTRLPDYLRGWQ
220 230 240 250 260 270 280
YKECCLQPEHTWQTHLSRQASGWLXVGLHGYAKCKPKGISRSFSLXHLXLLXELFXLSFDANSVQOILR
290 300 310 320 330 340 350
LEFLHVAQKQKNNKPEXKQWTVAPRYKCSGKRGHPASPHSAQSPSDORSPPRLYKLSFPOALHCH
360 370 380 390 400 410 420
SLSRRFFSLLSLQGLPGGILMMQENLRHCKRVGDHOKAKVPLILSQYCWPEGGHORAGVLSLISROPG
430 440 450 460 470
AASARAPAGPRRGPMRLGGGSSDRHSARFORPGSTPRAGSSSPG

LFEPFLKK
470

6. US-09-935-124A-2 (1-392)
US-09-935-124A-1 Sequence 1, Application US/09935124A

Sequence 1, Application US/09935124A
GENERAL INFORMATION:

APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Alchison, Robert
APPLICANT: Bogenberger, Jakob
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-000210us
CURRENT APPLICATION NUMBER: US/09/935,124A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: 60/284,760
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1422
TYPE: DNA
ORGANISM: Homo sapiens

Initial Score = 6 Optimized Score = 49 Significance = -0.42
Residue Identity = 188 Matches = 69 Mismatches = 213
Gaps = 95 Conservative Substitutions = 0
Translation Frame = 1

MDLPGDLPPEPSPRPAAGKEAQKGPLLPDDLPPASSTDSGSGGPLLPDDLPPASSGDSGLATSIQWVKT
10 20 30 40 50 60 70
GT
X
EGGAKRRTSEEEKSGSEELVEKVCCKA-----SSVIFGLKGYVAERKGEREMQDAHYIINDITE
80 90 100 110 120 130
RPAARAR-----PGCGARPLLAGXVVAASASTOPPPWTSGTCRSPSARARLPQKRLKRD-----
10 20 30 40 50
ECRPPSSLITRVSFAVVDGHG-----IRASKFAA---ONT--HONLRKFPKGDVISVEKTVK---CLL
140 150 160 170 180 190
---PCSLMT--SLRPAVLTDQDGLCFIMISHPLVALQVLLPHQYPRWXRLLKGEQREKPPRRKRMAYKSL
60 70 80 90 100 110 120
DTEKHTDEEFLK--QASSQKPA--MKDG-----STATCYLAVDNITLYIANLGDRAILCRYNESQ
200 210 220 230 240
WKRK-----FVAPLXSLVXRAMWLSGRVGRRCMPSTSTSPRSV-----GPHRPSL-----LG
130 140 150 160 170
KHAALSL--SKEHNFTOYERMRIRQKAGN-----VRDGRVLGVLEVSRSITGDQYKRCGVTSVP
250 260 270 280 290 300
PHLLFLMDMEFEFPONLHRCITXSENFLKEMXSVYRKPRDAFWTLSSILMKSSINKLPAKSLPGKW
180 190 200 210 220 230 240 250
DIRRCQLFNDRFLL--LACDGLFKYFTPEEAVNFIISGLEDEKIQTRREGKSAADARYEACNRLANKAVOR
310 320 330 340 350 360 370
PLPRVFWLXTTFEFLPTSEIVGQSCVIMRRVKNMQPKASAKSIITLSMKSGGYRLEETSGMGVFWACXR
260 270 280 290 300 310 320
380 390 X
GSADNVYVMVVRIGH
CHAPLGSTSAVAAPLCPTSDAASXPMPTGSCFPMVWGSSRLPQKKEPTSSCPVSRMKRSRPGKGSPOPT
330 340 350 360 370 380 390
PATKQPAWGMPTRBSGARPTTSLXWMCXGTEGWRBAASHTGIDLKSGFCVCAHCVCVFLIMDSHGCKKRF
400 410 420 430 440 450 460

[illegible]

```
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T18588; T21693
R:Mortimore, B.
submitted to the EMBL Data Library, December 1998
A:Reference number: Z18993
A:Accession: T18588
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-242 <W1>
A:Cross-references: EMBL:AL031264; PIDN:CAA20326.1; GSPDB:GN00020; CESP:F33A8.6
A:Experimental source: clone VF45E10L
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19459
A:Accession: T21693
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-242 <W12>
A:Cross-references: EMBL:Z81525; PIDN:CA804260.1; GSPDB:GN00020; CESP:F33A8.6
A:Experimental source: clone F33A8
C:Genetics:
A:Gene: CESP:F33A8.6
A:Map position: 2
A:Introns: 28/1; 65/2; 101/1; 133/2; 202/2

Alignment Scores:
Pred. No.:          3,61e-29           Length:      242
Score:             474.00            Matches:       98
Percent Similarity: 62.30%           Conservative:  54
Best Local Similarity: 40.16%         Mismatches:   80
Query Match:       18.52%            Indels:       12
DB:                2                 Gaps:         5

US-09-935-124A-1 (1-1422) x T18588 (1-242)

QY    345  TCCGAGGAAGAAGAAATGGCAGTGAAGCGTTG-----GAAAAGAACTT 392
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    3   SerApSerArGlYrArgSerSerxapApSerleuIeaPaSenSerApGlSerlyls 22

QY    393  TGTAAGCGCTTCGTGGTATCTTGCTGTGAAGGCGTATGCGCTGACCGGAGGCTGAG 452
      |||||:::|||||:::|||||:::|||||:::|||||:::
Db    23  ProLyvGlUSeArXgSmleuYrCyShrleuAlaIaTyrgLYCyArlyvsglylu 42

QY    453  AGGGAAGATGCAGATGCCACCAGCTCATCTCTGAAC-----GACATCACCGAGAGTGT 506
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    43  ArgAlaApMetGlnApThrHrlEtLeuNeuProLyvSphaApLeuGLyThrglu--- 61

QY    507  AGGCCCCATCGTCCCTCATTACTCGGGTTTCATATTGTTGCTGTTTTGATGACATGSA 566
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    62  -----LyserPheLeuSerArgLaSerPhePheAlaIlePheaSpGLYHIsAla 78

QY    567  GGAATTGCAAGCCTCAAAATTGGCTGCACAGAATTGCATCAAAACTTAATCAGAAAAATT 626
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    79  GlyPrOArGlaAlaIglnHiCygsGlnSerGlnMetGLyLyTrhValylsglulysleu 98

QY    627  CCTAAA---GGAGATGATATCAGTGTAGAGAAAACCGTAGAGAGATGCTTTTGACACT 683
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    99  AlalyvSpheserApPherProthrleuthrlyvsserleuLySGlnThrPheThrGlus 118

QY    684  TTCAGACATACTGATGAAGAAGTCTCTTAACAACGTTCCACCCACAGAACGCTGTGAAA 743
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    119  TyrLyvAlaValaAspAspGLyPheleuAlaIleAlaLyvSglnleuLyProIlleTryps 138

QY    744  GATGGGTCCACTGCACAGTGTGTTGGCTGTAGACAAATCTTTATATTGCCAACTC 803
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    139  AspglyThrThrAlaThrThrMetlleileuendAnValilleTyVAlaAlasnlle 158

QY    804  GGAGATAGTCGGGCGCATCTGTGCTGTTATATAGAGAGATCAAAAACATGACAGCTTGA 863
      |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db    159  GlyApSerArGlaValaValaIaArglyslvsglulaspGLY---SerPheAlaProVal 177

QY    864  ACCCTCAGAAAGACATATTCACATCAGATAGAAAGCGAGATGAGGATCAGAAAGCT 923
```

Db	178	CysLeuThrValAlaSerHisAspProMetSerHisAspGluValGlnMetAlaGlnIleGlnIlyValAla	197
Oy	924	GGAGAAACCTCGACGGGATGGGGCTGTTTGGGCGCTGAGAGGGTGCATGACGCTCATTTGGG	983
Db	198	GlyAlaValValIlyAspGlyArgIleAlaGlnIlyValIleGlnIlyValSerArgSerIleGly	217
Oy	984	GACGGGACATGATCAAGCGCTCCGGTGTACCTCTGTGCGCCGATCAACACGCTGCCAGCTG	1043
Db	218	AspLeuProPheIlySerLeuGlnIlyIleIleSerThrProAspLeuIlyIlyLeuThrLeu	237
Oy	1044	ACCCCATGAC	1055
Db	238	ThrIysAsnAsp	241
RESULT 3			
A:55804			
Phosphoprotein phosphatase (EC 3.1.3.16) 2c, membrane-bound - Paramedium tetraurelia			
C:Species: Paramedium tetraurelia			
C:Date: 23-Mar-1995 #sequence_rev:revision 05-Apr-1995 #text_change 07-Dec-1999			
C:Accession: A55804			
R:Klump, S.; Hanke, C.; Donella-Deana, A.; Beyer, A.; Keilner, R.; Pina, L.A.; Schultze			
J. Biol. Chem. 269, 32774-32780, 1994			
A:Title: A membrane-bound protein phosphatase type 2C from Paramedium tetraurelia. Purified			
A:Reference number: A55804; PMID:95105156; PMID:7806499			
A:Accession: A55804			
A:Status: preliminary			
A:Molecule type: mRNA			
A:Residues: 1-300 <RLU>			
A:Cross-references: GB:Z6985; NID:9537421; PID:e1192609; PID:g2654382			
C:Genetics:			
A:Genetic code: SGCS			
A:Keywords: phosphoric monoester hydrolase			
Alignment Scores:			
Pred. No.:	1,896-23	Length:	300
Score:	401.50	Matches:	102
Percent Similarity:	50.16%	Conservative:	53
Best Local Similarity:	33.01%	Mismatches:	105
Query Match:	15.68%	Indels:	49
Db:	2	Gaps:	9
US-09-935-124A-1 (1-1422) x A55804 (1-300)			
Oy	396	AAAGCCTCTTCGGTGATCTTGTGCTGAAGGGCTATGTGCTGACGGAGGGTGAGAG	455
Db	18	GlnIlyAspSerValIlePheAla-----AlaSerGlnMetGlnIlyTyrArg	33
Oy	456	GAGGAGATGAGGATGGCCACGTCATCTGACGACATCACCGAGGAGTGAAGCCCCCA	515
Db	34	AsnThrMetGlnLeuPalaHisIleHisArgHisAspIleIleGlnAsp-----	49
Oy	516	TGCGCCCTCATCTCTGCGGTTTCATATTTTGTGCTTTTGAATGACATGAGGAAATTCGA	575
Db	50	-----ValSerValPheGlyValPheAspGlyHisGlyIlyAspGln	63
Oy	576	GGCTCAAAATTTGCTGACAGATTTGCATCAAAATTCATATTC-----AGAAATTTCT	629
Db	64	ValAlaGlnPheValGlnIlySerHisPheValAspGlnLeuIlySerIlyAsnIlyPheIly	83
Oy	630	AAAGAGATGTAATCACTGTAGGAAACCGTGAAGAATGCTTTTGACACATTTCAG	689
Db	84	-----GlnGlnIlySerPheGlnGlnIlyAlaLeuIlySerGlnIlyPheLeu	96
Oy	690	CATCTGATGAAAGATTCTT-----AAACAAGCTTCCAGCCGAAGCCT	734
Db	97	LysMetSerAspGlnLeuLeuLeuThrProGlnIlyGlnIlySerGlnLeuAsnGlnIlyTyrIlyValAla	116
Oy	735	GCCTGAAAGAT-----GGTCCACTGCCACGTGTGTTCTTGCGCTGATGACAC	782
Db	117	ThrAspThrAspGlnSerTyrAlaGlnIlyCysThrIlyAlaAsnValAlaLeuIlyTyrIlySer	136
Oy	783	ATTCCTATATATGCAACCTCGAGATAGTCGGAGCAATCTTGTGCTTAAATAGAG	842

QY 620 AAAATTCTTAAAGAGATGTAATCAGTGTAGAGAAAACCTGAAGAGATCCCTTTTGA 679
 Db : |||||
 Db 772 nserpheargapglyasp-----Tyruglnalnapeargas 785
 QY 680 CACTTTCAGCATCTACTGAGAGATTCTTAAACAGCTTCACAGACCTGCTG 739
 Db : |||||
 Db 785 palatyratalaualapaspillevalliegulyscysgu----- 799
 QY 740 GAAAGATGGGTCCACTGCCACGTGTGTTGCTGTAGACACATTTTATATGCAA 799
 Db : |||||
 Db 800 -lysergiysertthrglyvalseralaleuleuvalgllyanlyserlythrinala 819
 QY 800 CCTCGAGATGTCGGGCAATCTTGTCTTAAATGAGAGAGCTCAAAAACATGACG 859
 Db : |||||
 Db 819 nvalgllyaspsersguillevallleaualaglnalproanalaasnp-rolysglyr 839
 QY 860 CTTAAGC-----CTCAGCAAAAGACATACTCACTAGTATGAAAGCG 904
 Db : |||||
 Db 839 ovalthrlyrgluprovalleuleuserlyrlyshlsleualaseraspapnglnly 859
 QY 905 GATGAGATACAGAAAGCTCGAGAGAACCTCAGGAGTGGGCTGTTTGGCGCTGAC 964
 Db : |||||
 Db 859 slysargvalthrnapleuglygmelllelpeasnapleupheglyserleual 879
 QY 965 GGTGTACGCTCCATTGGGACCGGACATCAAGCC-----TCCGCTGT 1009
 Db : |||||
 Db 879 avalsersarserpheglyaspysglutrylsglnlygllystysphecys----- 897
 QY 1010 CACTCTGTGCCGACATCAGACCTGCGACCTGACCCCAATGACAGTTTCATTTGT 1069
 Db : |||||
 Db 898 -valsersp-roltyrglnthrthrthrnapleuthralaagasphepellele 917
 QY 1070 GGCTGTGATGGGCTCTTCAAGGCTTTATCCCAAGAAAGACCGGAACTTCATCTTGT 1129
 Db : |||||
 Db 917 ualacysaspnglyleutrpaspysvalglutryraspdlualalvalglnpheval----- 935
 QY 1130 CTGTCTCGAGATGAAAGATCCAGCCCGGAGGAAGTCCGACCGGACGCGCGCTA 1189
 Db : |||||
 Db 936 -----Glnargasnilleysleuglyysersalathrglu----- 947
 QY 1190 CGAAGACGCTGCACACAGCGTGGCCACCAAGCGCGTGCAGCGGCTGCGCCGCAACGT 1249
 Db : |||||
 Db 948 -----llesergluleuleualaglnaspsertyraspdpaglysergllyasphenil 965
 QY 1250 CACTGTGATGCTGTG 1265
 Db : |||||
 Db 965 etnrtalaleuvalval 970
 RESULT 6
 T05095
 hypothetical protein F28M20.60 - Arabidopsis thaliana
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
 C/Accession: T05095
 R/Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hohelsel, J.; Mewes, submitted to the Protein Sequence Database, November 1998
 A/Reference number: Z15398
 A/Accession: T05095
 A/Molecule type: DNA
 A/Residues: 1-389 <BEV>
 A/Cross-references: EMBL:AL031004
 A/Experimental source: cultivar Columbia; BAC clone F28M20
 C/Genetic:
 A/Map position: 4
 A/Intons: 95/1; 128/1; 181/1; 210/1; 274/3; 318/3
 A/Note: F28M20.60
 C/Superfamily: human phosphoprotein phosphatase 1A
 Alignment Scores:
 Pred. No.: 8.6e-21 Length: 389
 Score: 368.00 Matches: 114
 Percent Similarity: 45.56% Conservative: 40
 Best Local Similarity: 33.73% Mismatches: 86

Query Match: 14.37% Indels: 98
 DB: 2 Gaps: 14
 US-09-935-124a-1 (1-1422) x T05095 (1-389)
 QY 426 GGTATGTGGCTGAGCGGAAGGGTGAAGAGAGATGACAGATGCCACGTCTCCTG 485
 Db : |||||
 Db 60 GlyTyr---AlaserserProglylybarsersermetcunaspheylrglnthrarg 78
 QY 486 AACGATCACCCAGAGATGTAGCGCCCATCGTCCCTCATTCCTGGGTTTCATATTT 545
 Db : |||||
 Db 79 lilepvalgllyglly-----Glnllevalgllyneuphe 90
 QY 546 GCTATTGTTTATGATGAGATGAGAAATTCAGACCTCAAAATTCGTCGACAGAAATTCAT 605
 Db : |||||
 Db 91 GlyValpheaspilyselglylvalahpvalaleglutryvallyselinsneuphe 110
 QY 606 CAAAATTATCGAAAATTTCTTAAAGAGATGATACAGTGTAGAGAAAACCTGAG 665
 Db : |||||
 Db 111 Serenleullearg---HisProlys-----PheIleaser---AspThrThr 124
 QY 666 AGATGCTTTTGGACACTTCAAGCATCTGTAGAGAGATTCTTAAACAGCTTCCAGC 725
 Db : |||||
 Db 125 AlaIallealaspalatyrsanglnthrapsersrlupheuleuserglunaser 144
 QY 726 CAGAAAGCTGCTGGAAGAT---GGGTCACTGCCACGTGTGCTGCTGTAGACAAAC 782
 Db : |||||
 Db 145 Glnasn-----Argaspalaglyserthralseserthrallaleuvalgllyasp 161
 QY 783 ATTCTTATATTCGCAACCTCGAGATAGTCGGCAATCTTGTGCTTATATGAGAG 842
 Db : |||||
 Db 162 Argleuleuvalalaspvalgllyaspserargvalalaleysarglygllyasn--- 180
 QY 843 AGTCAAAACATGACACCTTAAAGCTTCAGCAAGAAAGATATTCACACTCAGATATGAG 902
 Db : |||||
 Db 181 -----Alallealvalaserargasphepshysp-rolasp-rolinsersp-rol 195
 QY 903 CGSAGAGATACAGAGGCTGAGAGAAAGCTGACG-----GATGGGCTGTTTGTG 953
 Db : |||||
 Db 186 Argglnarglleglunaspaleglylphelvalmetcrlphaleglythrtrpargvalglly 215
 QY 954 GCGGTGCTAAGATGTGACAGCTTCATTTGGGAGACGGGACATCAAGCGCGCTGACCC 1013
 Db : |||||
 Db 216 GlyValleuvalalaserargalphegllyasprgleuleuleuysglintyr---Valval 234
 QY 1014 TCTGTGCCGACATCAGA----- 1031
 Db : |||||
 Db 235 AlaspProglutlleglnvalleuthrPheCysGlnasneuleuleuTyrilleysasn 254
 QY 1031 ----- 1031
 Db 255 Alathrleuleuethrilleglunhisasnleuhsrtrilleserillevalserlyleu 274
 QY 1032 -----CGTGCAGCTGACCCCAATGACAG----- 1058
 Db 275 Aenglythrleuglnasnphelneuprgserleulleserilleasnlylsrphenglnlu 294
 QY 1059 -----TTCAATTGTTGGCTGTGATGGCTGTTCAGAGTC 1094
 Db : |||||
 Db 295 Glutysvalnapserserleuglnubheuleuleuleuilaaseraspilyleutrpaspval 314
 QY 1095 TTTACCCCAAGAAAGCGTGAACCTTCATCTTGTCCGTGTCGAGGATGAAGATTCAG 1154
 Db : |||||
 Db 315 Valserasnlglnalvalalgllymetlle---lysallaleglunasp-rol 330
 QY 1155 ACCCGGAGAGGAAGTCCGACACCGACCGCCGCTACAGAACCTTCGACAGCGTGGCC 1214
 Db : |||||
 Db 331 -----Glnuglnlyalalyahrgneumet 338
 QY 1215 AACAGCGGTGACAGGGGCTGCGCCGACACAGCTCAGTGTATGTGGTGGG 1268
 Db : |||||
 Db 339 MetglnalatyrglnargglyseralaspasnillethrCysvalalvalarg 356

RESULT 7

phosphoprotein phosphatase [EC 3.1.3.16] 2C [imported] - common ice plant
C:Species: Mesembryanthemum crystallinum (common ice plant)
C:Date: 24-Oct-2000 #sequence revision 24-Oct-2000 #text_change 01-Mar-2002
C:Accession: T52337
R:Myazaki, S.; Koga, R.; Bohner, H.U.; Fukuhara, T.
Mol. Gen. Genet. 261, 307-316, 1999
A:Title: Tissue- and environmental response-specific expression of 10 PP2C transcripts
A:Reference number: Z66045; MUID:99200489; PMID:10102366
A:Accession: T52337
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-359 <MI>
A:Cross-references: EMBL:AF075580; PIDD:AMC36698.1
C:GeneticS:
A:Gene: PP2C
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220
C:Keywords: phosphoric monoester hydrolase

[illegible]

Qy	447	GGTAGAGGAGGAGAGATCSAGAGATGCCCAAGTCATCTCTAAACAGATCAACCGAGAG---	503
Db	58	GlyProArgLysTyrMetGlnAspGlnHisIleArgLysAspSerLeuValGlnLeu	77
Qy	504	-----TGTAGGCCCCCATCTCCCTCCATTTACTCGGGTTTCATATTTGGCT	548
Db	78	GlySerLeuPheArgCysProIysProSer-----AlaPheTyrGly	91
Qy	549	GTTTGTGATGAGCACTGGAGAGATTCGAGCCTCAAAATTGCTGCACAGAAATTTGCATCA	608
Db	92	ValPheArgGlyHisGlyGlySerGlnAlaIleAlaTyrValArgLysIleAsnValMetArg	111
Qy	609	AACTTAATCAAG-----AAATTTCCCAAGGA-----GATTTAATCAGTGGAG	653
Db	112	PhePhePheGlnAspValSerPheProGlnAlaSerGlnLeuAspGlnIlePheLeuGln	131
Qy	654	AAAACCGTGAAGAGATCCTTTTGGACACTTTCAAGCATCATGATGAAGATTTCTTTAA	713
Db	132	--GlyValGlnAsnCysLeuArgArgAlaPhePheLeuAlaAsp-----LeuAla	147
Qy	714	CAAGCTTCACAGCCGAAGCCTGCTGGAAAGATGGGTCCACTGCCACGTGTCTTGCGCT	773
Db	148	LeuAlaAspAspCysSerIleSerThrSerSerGlyThrThrAlaLeuThrAlaLeuVal	167
Qy	774	GTAGACAACATCTTTTATTATGTCACAACTCGAGATAGTGGGACATCTTGTCGTAT	833
Db	168	LeuGlnArgLeuLeuLeuValAlaAsnAlaGlyAspCysArgAlaValAlaLeuCysArgLys	187
Qy	834	AATGAGAGACTCAAAAACATGCAGCCTTAAGCCTCAGCAAGAGCATATCAACTCAG	893
Db	188	GlyGln-----AlaIleAspMetSerGlnAspHisArgProThrTyr	201
Qy	894	TATGAAGCGGATGAGGATACAGAAAGCTGGAGGAAGCATCGGATGGGCGTGGTTG	953
Db	202	ProSerGlnLysValArgValGlnGlnLeuGlyGlyTyrValAspAspGlyTyrLeuAsn	221
Qy	954	GGCGTGTAGAGGTGTCAACGCTTCATTTGGGGAAGGCGCATGACAG-----	998
Db	222	GlyAlaLeuSerValSerArgAlaLeuGlyAspTrpAspMetLysLeuProLysGlySer	241
Qy	999	CGCTCGCGGTCACTCTGTGCCCCGACATACAGAGCTGGCCAGTGAACCCCATATGACAG	1056
Db	242	AlaSerProLeuIleSerGlnProGlnLeuArgGlnIleIleLeuThrGlnLysAspGln	261

[illegible]

RESULT 8
150783
protein phosphatase 2C-like protein - *Arabidopsis thaliana*

A:Map position: 5
A:Intons: 27/2; 70/1; 103/1; 156/1; 185/1; 209/3; 234/3
A:Note: T3ON20 10
C:Superfamily: _human phosphoprotein phosphatase 1A

Alignment Scores:		
Pred. No.:	1,58e-20	Length: 34
Score:	364.50	Matches: 10
Percent Similarity:	53.00%	Conservative: 86
Best Local Similarity:	36.40%	Mismatches: 17
Query Match:	14.34%	Indels: 43
GB:	2	Gaps: 13

US-09-935-124A-1 (1-1422) X T50783 (1-348)

QY	426	GGCTATGTGCTGAGCGGAMGGGTGAGAGGAGATGCAAGAT--GCCACGTCATC	482
Db	35	GlyTyr---AlaSerSerAlaGlyValArgSerSerMetGluAspPheGluThrArg	53
QY	483	CTGAACGACATCACCAGAGAGGTGAAGGCCCCCATCGCTCCTCATTAATCGGGTTTCATAT	542
Db	54	IleAspGlyIleAsnGlyGluIle-----ValGlyLeu	64
QY	543	TTTGCTGTTTTTGAATGACATGTAGAGAAATTCAGAGCCTCAAAATTTGCTGCACAAATTTG	602
Db	65	PheGlyValIlePheAspGlyIleSgIleValAlaArgAlaAlaGluIleValValValGlnIleLeu	84
QY	603	CATCAAACTTTAATCAGAAAAATTTCTTAAAGAGATGTAACTAGGTGAGAAAAACCGTG	662
Db	85	PheSerAsnLeuIle---ThrHisProIys-----PheIleSer-----AspThr	98
QY	663	AAGAGATGCTTTTGGACACTTTTCACAGCATACTGATGAGAAGATTTCTTTAAACAAGCTTCC	722
Db	99	LysSerAlaIleThrAspAlaIleValAsnHisThrAspSerGluLeuLeuLysSerGluAsn	118
QY	723	AGCCGAAGACCTGCGCTGAAAGAT---GGTCCATCGGCCACGTCGTCTTCGCGCTGTAGAC	779
Db	119	SerHisAsn-----ArgAspAlaGlySerThrHisIleSerThrAlaIleLeuValGly	135

QY 780 AACATCTTTATATTCGCAACCTGAGATAGTCGGGCAATCTGTCTGTTAAATGAG 839
 Db 136 AAspArgLeuValAlaIleValAlaSerValGlyLeuValLeuValSerValGlyLeuVal 155
 QY 840 GAGAGTCAAAAACATGACGCTTAAAGCTTCAGCAAGAGCAATATTCGAATGAA 899
 Db 156 -----AlaIleAlaValSerValAspValProAspGlnSerAsp 169
 QY 900 GAGCGATGAGGATACAGAGCTGAGAGAAAGCTCAGGATGGCGTGTGGCGCTG 959
 Db 170 GluArgGluArgIleGluAsnAlaGlyGlyPheVal-----MetTrpAlaGlyVal 186
 QY 960 CTAGAGGTGTCAGCTCCATTCATTCGAGCGGACAGTAAAGCTGCGTGCATCCTGCG 1019
 Db 187 LeuAlaValSerValGlyPheGlyAspArgLeuValGlnTyr-----ValValAlaAsp 205
 QY 1020 CCGGACATCAGACGCTGCGACGCTGACCCCAATGAGAGCTTCATTCGCTGTGAT 1079
 Db 206 ProGluIleGlnGluGluValIleAspAspThrLeuGluPheLeuIleValAsp 225
 QY 1080 GGGCTCTCAAGCTTTTACCCAGAAAGAGCTGACCTTCATCTGTCTGTCGAG 1139
 Db 226 GlyLeuTrpAspValPheSerValSerValAlaValAlaMetVal----- 240
 QY 1140 GATGAAGATCCAGACCCGGAGAGGAGTCCGACCCGACCCCTGACGAAAGACC 1199
 Db 241 -----LysGluValGluAspPro-----GluAspSer 249
 QY 1200 TGCACAGGCTGCGCAACAGCGGTCAGCGGCTCGCGGCAACGTCACGTGATG 1259
 Db 250 AlaValLeuValGlyGluAlaIleValArgIleValAspAsnIleThrCysVal 269
 QY 1260 GTGGTGGCG 1268
 Db 270 ValValArg 272
 RESULT 9
 S54297
 protein phosphatase 2C homolog - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 15-Jun-2001
 C:Accession: S54297; T40871
 P:Shiozaki, K.; Russell, P.
 EMBL J 14, 492-502, 1995
 A:Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase kinase hc
 A:Reference number: S54297; MUID:95163582; PMID:7859738
 A:Accession: S54297
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-370 <SNR>
 A:Cross-references: EMBL:L34881; NID:G609655; PIDN:AAA67320.1; PID:G609656
 R:Wedler, H.; Wambut, R.; Lyne, M.; Rajandream, M.A.; Barrett, B.G.
 submitted to the EMBL Data Library, September 1998
 A:Reference number: Z21953
 A:Accession: T40871
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-370 <MED>
 A:Cross-references: EMBL:AL031579; PIDN:CAA20880.1; GSPDB:GN00068; SPDB:SPCC1223.11
 A:Experimental source: strain 972h-; cosmid c1223
 C:Genetics:
 A:Gene: SPCC1223.11
 A:Map position: 3
 C:Superfamily: human phosphoprotein phosphatase 1A
 Alignment Scores:
 Pred. No.: 2.57e-20 Length: 370
 Score: 362.00 Match: 107
 Percent Similarity: 47.68% Conservative: 47
 Best Local Similarity: 33.13% Mismatches: 110
 Query Match: 14.14% Indels: 59
 Db: 2 Gaps: 14

US-09-935-124a-1 (1-1422) x S54297 (1-370)
 QY 407 GTCATCTTTGCTTGAAAGGCTATGTGCTGAGCGGAGGTGAGAGGAGATGCA 466
 Db 18 GlyAspArgTrp-LeuHisPheGlyValSerHisMetGlnGlyTrpArgIleSerMetGly 37
 QY 467 GGAATGCCAGCTATCCTGAAAGCATCAGAG-----GAGTGAAGGCCCCATGCT 520
 Db 37 uAspAlaHisCysAlaIleLeuAsnPheThrAspSerValSerSerAspProProth-- 56
 QY 521 CCTCATTAACGCGGTTTATATTTGCTTTTGTATGATGACATGAGAGATTCGAGCTC 580
 Db 57 -----SerPhePheGlyValPheAspGlyHisGlyGlyAspArgValAl 71
 QY 581 AAAATTGCTGCACAGATTTGTCATCAAACTTAAATGAGAAATTTCCT-----AA 631
 Db 71 alytyrCysArgGlnIleLeu-----ProAspIleIleIleValSerGlnProSerPheTrp 90
 QY 632 AGGAGATGTAATACGTGTAGAGAAAACCTGAGAGATGCTTTTGACACATTCAGCA 691
 Db 90 sGlyAsn-----TyrAspGluAlaLeuLysSerGlyPheVal 103
 QY 632 TACTGATGAAGATTCCTTAAACAAGCTTCAGCGAGAGCTGCGTGAAGATGGCTC 751
 Db 103 aAlaAspAsnAlaLeuMetGlnAspArgAspMetGlnGluAsp-----ProSerGlyCys 121
 QY 752 CACTGCCACGCTGTGTTCTGCTGTGACAAAC--ATTCTTATATTCGCAACCTCGAGA 808
 Db 121 sThrAlaThrThrAlaLeuIleValAspHisGlnValIleTyrCysAlaAsnAlaGlyLeu 141
 QY 809 TAGTCGGGCATCTTGTCTGTTATTAAGAGAGAGTCAAAAATGACGCTTAAGCT 868
 Db 141 pSerArgThrValLeuGluArg-----LysGlyThrAlaGluProLe 155
 QY 869 CAGCAAGAGCATTAATCCAACTCAGTATGAGAGCGGATGAGATCAGAAAGCTGAGG 928
 Db 155 uSerPheAspHisIleValProAsnAsnAspValGlyValAlaArgIleThrAlaAlaGly 175
 QY 929 AAAGTGAAGGATGGGCGTGTGTTGGCGCTGACAGGTGTACGCTCATTCGCGGAGG 988
 Db 175 yPheIleAspPheGlyArgValAsnGlySerLeuAlaLeuSerValAlaIleGlyAspPh 195
 QY 989 GCATTCACAAAGCGCTGGCT-----GTACCTCTGTGCTCCGA 1024
 Db 195 eGluTrpLysLysAspSerSerLeuProGluLysGlnIleValThrAlaPheProAs 215
 QY 1025 CATCAGAGCTGCGACGCTGACCCCAATGACAGGTTCACTTGTGCTGTGATGGCT 1084
 Db 215 pValValIleHisAsnIleAspProAspAspGluPheLeuIleLeuAlaCysAspGlyI 235
 QY 1085 CTTCAGAGCTTTATCCCGAGAGAACCCGTAACCTTCATCTGTGCTGTGAGATGA 1144
 Db 235 eTrpAspCysLysSerSerGlnGlnValValGluPheVal----- 248
 QY 1145 AAAGATCAAGACCCGGAGAGGAGAGTCCGACGCGGACGCGCTACAGACGCTGCA 1204
 Db 249 -----ArgArgGlyIleValAlaArgGlnSer-----LeuGluValIleCysGly 263
 QY 1205 CAGGCTGCGCAACAGGCGTACAGCGGCGCTG-----GCCGACAA 1246
 Db 263 uAsnLeuMetAspArgCysIleAlaSerAsnSerGluSerCysGlyIleGlyCysAspAs 283
 QY 1247 CGTACGTGATGCTGTGTCGGATGAGGCACTAGAGGCTGCGCGGACAGAGCAAGC 1306
 Db 283 nMetThrIleCysIleValAlaPheLeuHis-----GlyArgGlyLeuGluAsp-- 299
 QY 1307 ATGTGAT 1313
 Db 300 -TrpTrp 301
 RESULT 10
 H96700
 protein F12A21.5 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H96700
 R:Theologos, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.;
 Hansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Author: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiz, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Author: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 Article: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96700
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-464 <STO>
 A:Cross-references: GB:AE005173; NID:g11072032; PIDN:AA628911.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: P12A21.5
 A:Map position: 1
 Alignment Scores:
 Pred. No.: 2,66e-20 Length: 464
 Score: 362.00 Matches: 108
 Percent Similarity: 45.26% Conservative: 59-
 Best Local Similarity: 29.27% Mismatches: 104
 Query Match: 14.14% Indels: 98
 Gaps: 13

US-09-935-124a-1 (1-1422) x H96700 (1-464)

QY 405 TCGGTGATCTTGGTCTGAAGGCTAT---GTGGCTGAGCGAAGGCTGAGGAGAG 461
 DB 113 ThrValSerPheIleValGlnGlyPheGlyValValSerArgSerMetGlyValSerPhe 132

QY 462 ATGCAGATGCCCGCATCTGTAAGCATCAGCATCCGAGAGATGAGGCCCCCATGCTCC 521
 DB 133 MetGluAspThrHisArgIleVal-----ProCysIleValGlyGlnAsnSer 147

QY 522 CTCATTACTCGGGCTTCATATTTTGTCTGTTTGTATGATGACATGAGAAATTCGAGCTCA 581
 DB 148 -----LysIleSerPhePheGlyValTyArgPglYHisIleGlyIleValalaala 164

QY 582 AATTGTCGCAGAAATTTGATCAAACTTAATGAGAAATTTCT-----AAAGA 635
 DB 165 GluPheValAlaGluAsnLeuHisIleValTyValValGluMetCyluAsnCyluValGly 184

QY 636 GATGTATCATGTGTAGAGAAACCGTGAAGAGATGCTTTTGACACTTTCAAGCATACT 695
 DB 185 LysGluGluLysValGlu-----AlaPheLysAlaIlePheLeuArgThr 199

QY 696 GATGAAGACTTCTTAACAGAGCTCCAGCCAGAGCTGCTGGAAGATGGGTCCTCACT 755
 DB 200 AsparGAspPheLeuLysValIleValIleLysGluGlnSerLeuValValSerGly 219

QY 756 GGCACGTGTTCTGGCTGT-----GACAATCTTTATATTCGCAACTCCGAGAT 809
 DB 220 AlaCysCysValThrAlaValIleGlnAspGlnGluMetIleValSerAsnLeuGlyAsp 239

QY 810 AGTCGGGCAATCTTGTGTCTTTATATGAGAGAGTCAAAAACATGACGCTTAAAGCTC 869
 DB 240 CysArgAlaValLeuLeuValArgIleVal-----ValAlaGluAlaLeu 253

QY 870 AGCAAAAGACATATCAACTCATGTATGAGAGCGGATGAGATACAGAG----- 920
 DB 254 ThrAspAspHisIleValArgPglTyArgAspArgGluValGluIleGluSerGlnSerLeu 273

QY 921 -----GCTGAGGAAAGCTCAAGGAT-----GGG 944
 DB 274 IleProPheMetThrPheGlyLeuGlnGlyTyValValAspAsnHisGlnGlyAlaTyr 293

QY 945 CGTGTGTTGGCGGTCTAGAGGTGTACAGCTTCATTTGGGAGCGGACATCAAGCGCTGC 1004
 DB 294 ArgValGlnGlyIleLeuAlaValSerArgSerIleGlyAspAlaHisIleValLeuValSer 312

QY 1005 GGTGTACCTCTGTGTCGGACATGACAGCTGCCAGCTGACCCCCAATGACAGCTTCATT 1064
 DB 313 ThrValValAlaGluProGluThrArgValLeuGluLeuGluGlnAspMetCyluLeu 332

QY 1065 TTGTTGGCTGTGATGGCTCTTCAAGGCTTTACCCGAAAGAGCCGTGAATTTCATT 1124
 DB 333 ValLeuAlaSerAspGlyLeuThrAspValValSerAsnGlnGluAlaValTyThrVal 352

QY 1125 TTGCTCTGCTC-----GAGCATGAAAAATCCAG 1154
 DB 353 LeuHisValLeuAlaGlnArgTyThrProLysGluSerGluGlnGluValGln 372

QY 1155 -----ACCGGGAAGGG 1166
 DB 373 GlyPheValAsnMetSerProSerSerLysLeuArgAlaSerLeuValLysSerPro 392

QY 1167 AGTCCCGACCGCAGCCCGCTAC----- 1190
 DB 393 ArgCysAlaLysSerGlnSerTyTyTyThrAsnSerGluAsnGluSerProSerLeuAsn 412

QY 1190 ----- 1190
 DB 413 ArgGluIleGlySerSerProSerLysSerProIleThrProTyLysSerLeuThrAla 432

QY 1191 GAGCAGACCTGTGAACAGCTGCGCCACAAGCGGTGCGAGCGGCTCGGCGCAACAGTC 1250
 DB 433 LysAlaAlaCysLysGluLeuAlaAsnLeuAlaLysAlaLysArgGlySerMetAspAspIle 452

QY 1251 ACTGTGATGTGTGTCGATGAGGAC 1277
 DB 453 ThrValValIleIleIleAspLeuAsnHis 461

RESULT 11
 T00750
 probable protein phosphatase 2C [imported] - Arabidopsis thaliana
 N:Alternate names: hypothetical protein T20B5.6
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
 C:Accession: T00750; G84834
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL Data Library, November 1997
 A:Description: Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence.
 A:Reference number: Z14159
 A:Accession: T00750
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-404 <ROU>
 A:Cross-references: EMBL:AC002409; NID:g2623294; PID:g2623300
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanden, S.E.; Umayam, L.; Tallon, L.;
 esen, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617157
 A:Accession: G84834
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-404 <STO>
 A:Cross-references: GB:AE002093; NID:g2623300; PIDN:AA86446.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: T20B5.6; At2g40860
 A:Map position: 2
 A:Introns: 178/1; 200/2; 273/3; 308/3; 340/3
 Alignment Scores:
 Pred. No.: 3.37e-20 Length: 404
 Score: 360.50 Matches: 127
 Percent Similarity: 41.82% Conservative: 57

Best Local Similarity: 28.86% Mismatches: 137
 Query Match: 14.08% Indels: 119
 DB: 2 Gaps: 17

US-09-935-124a-1 (1-1422) x T00750 (1-404)

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QY 84 CTCAC---CCAGCTCCGACATGACCTTTGCGGGACCTGCGGACCCGACCCGAC 140
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 26 LeuH1aLeuProlyserLeuSerLeuSerLeuSerLeuSerLeuSerLeuSerLeu 45
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 141 CCGCGCCCGGCTGCC----- 155
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 46 LysArgProSerSerAspAsnValValLeuGluLeuGluSerLeuTyrGluGlnValArg 65
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 156 GGGAAAGAAAGCTCAGAAAGACCCCTGCTTTGATGACCTCCCTCCGCGACAGACT 215
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 66 GlyLys-----GlnGlnGlyLeuLeuGlnLysLysSerLeuSerLeuSerLeu 83
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 216 GACTCAGATCAGGGGACCTTTGCTTTGATGATCTCCACCCGCTAGAGAGAGAT 275
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 84 Asp-----GlyAlaSerLeuLeu-----LysAsnSerGlyAsp 94
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 276 TCAGCTCTCTTCCACATCAATCTCCAGATGTAAAGATGAAAGGAAAGACAAAG 335
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 95 TyrArgAspThrValAsnTyrPheSerGln-----GlyGluCysLeuSer 109
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 336 AGAAAACTCCGACGAAAGAGAGATGCGAGTAAAGCTTGGAAAAAGAAAGTTTGT 395
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 110 LysLysSerSer----- 113
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 396 AAGACCTCTTGGTATCTTGTATGAAAGGCTATGCTAGACCGGAG----- 446
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 114 -----ValSerThrValPheAspValLysLeuTyrSerSerSerThrAspGluProSer 131
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 447 ----- 464
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 132 ArgTyrValProValIleSerCysGlySerPheAlaThrCysGlyLysArgGluSerMet 151
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 465 CAGGATGCCACGATCTGATCAAGATGACGACGAGTGAAGCCCATGCTCCCTC 524
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 152 GluAspThrHisPheIleIleProIleMetCysAsnGln----- 164
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 525 ATTAGTCGGGTTTCATATTGCTGTTTGTATGATGACATGACGAAATTCGAGCTCAAA 584
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 165 ---GluSerIleHisLeuPheHisIlePheAspGlyHisAspGlyAlaAlaAlaGln 183
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 585 TTTCGTGACAGATTTGACATCAAAACTTAAATGAAATTTCCCTAAAGAGATGATC 644
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 184 PheSerHisGlnValLeu-----ProGlyLeuValGln 194
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 645 AGCTGAGAGAAAAC---GTGAGAGATGCTTTTGACACATTTGACAGATATCTGATGA 701
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 195 SerLeuSerSerThrSerHisGlyGluAlaLeuSerGlnAlaPheValArgThrAspLeu 214
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 702 GAGTTCCTTAAACAGCTTTCAGGACGAGACCTGCC-----TGG 740
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 215 AlaPheArgGlnGluLeuAspSerHisAspGlnSerLysArgValSerGlnLysAspTyr 234
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 741 AAGATGGCTCAGCTGACGACGCTGTTCTGCTGTAGACACATTTTATATATGCCAAC 800
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 235 HisProGlyCysThrAlaIleAlaSerLeuLeuValGluAsnLysLeuPheValAlaAsn 254
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 801 CTCGAGATAGTCGGGCAATCTTGTGCTGTTATATGAGAGAGATCAAAAACATGACGCC 860
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 255 ValGlyAspSerArgAlaIleLeuCysArgAlaGlyHis-----Pro 268
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 861 TTAAAGCTCAGACAAAGACATATCAATCAATGATTAAGAGACGAGATGAGATCAGAG 920
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 269 PheAlaLeuSerLysAlaHisLeuAlaThrCysIleAspGluAspAsnValIleGly 288
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 921 GCTGAGGAAAGCTCAGG-----GATGGCGTGTGTTGGCGGTG---CTAGAG 965
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 289 GluGlyGlyArgIleGluTyrPheValAspThrTyrAspValAlaProAlaGlyLeuGln 308
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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QY 966 GTGTACGCTTCATTTGGGAGCGGGACGATCAAGCGCTCGCGGTGACCTCTGTGCGCGAC 1025
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 309 ValHisArgSerIleGlyAspAspAspLeuLeuPro---AlaValThrAlaGluProGlu 327
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1026 ATCAGACGCTGACGCTGACCCCAATGACAGCTTCAATTTTGTGCGCTGTGATGGCTC 1085
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 328 IleSerGlnThrIleLeuSerAlaAspAspGluPheLeuValMetAlaSerAspGlyLeu 347
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1086 TTCAAGCTCTTTACCCAGAGAAAGCGGTGAATCTTCACTCTGCTCTCGAGAGTAA 1145
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 348 TrpAspValMetAspAspGluGluValIleGlyIleIleArgAspThrValLysGluPro 367
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1146 AAGATCCAGACCCGGGAGACGAGATGCCAGCGGACCGCGCTACGAAAGACGCTGCAAC 1205
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 368 SerMetCysSerLys----- 372
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1206 AGGCTGCGCAACAAAGCGGTGACGCGGGGCTCGGCGGACAGCTCATGTATGATGGTGT 1265
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 373 ArgLeuAlaThrGluAlaAlaAlaArgGlySerGlyAspAsnIleThrValIleValVal 392
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
 T45778
 protein phosphatase 2C-like protein - Arabidopsis thaliana
 M:Alternate names: protein P26013.110
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_rev1501 04-Feb-2000 #text_change 03-Jun-2002
 C:Accession: T45778
 R:Deisemy, M.; Berger, C.; Cooke, R.; Grelliec, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.;
 submitted to the Protein Sequence Database, December 1999
 A:Reference number: Z23013
 A:Accession: T45778
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-361
 A:Cross-references: EMBL:AL13452
 A:Experimental source: cultivar Columbia; BAC clone P26013
 C:Genetics:
 A:Map position: 3
 A:Introns: 49/3; 108/3
 A:Note: P26013.110
 C:Superfamily: Arabidopsis thaliana hypothetical protein P7A7.220

Alignment Scores:
 Pred. No.: 4,71e-20 Length: 361
 Score: 358.50 Matches: 86
 Percent Similarity: 51.25% Conservative: 58
 Best Local Similarity: 30.68% Mismatches: 96
 Query Match: 14.00% Indels: 41
 DB: 2 Gaps: 8

US-09-935-124a-1 (1-1422) x T45778 (1-361)

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QY 444 AAGGTGAGAGGAGGAGATGACGATGCCAGCTCAATCTGAAACATCACCGAGAG 503
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 79 LysGlyProLysGlnSerMetGluSerGluPheIleCysValAspAspLeuThrGlyTr 98
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 504 TGTAGGCCCCATCGCTTCATTTCTGCGGTTTCATATTTGCTGTTTGTATGACAT 563
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 99 IleGlySerSerThrGly-----AlaPheThrGlyValPheAspGlyHis 113
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 564 GAGGAAATTCGACCTCAAAATTTGCTGACAGCAATTTGCATCAAAATTAATC----- 617
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 114 GlyGlyValAspHisAlaSerPheThrIleValSerHisIleMetLysLeuValMetGluAsp 133
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 618 AGAAATTTCTTAAAGAGATGTATCAGTGTAGAGAAACCGTGAAGAGATGCTTTTG 677
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 134 LysHisPhePro-----ThSerThrLysValAlaThrArg 145
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
QY 678 GACACTTTCAAGATCTGATGAGAGATTTCTTAAACAGACTTCGACGAAAGCTTGGC 737
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 146 SerAlaPheValLysThrAspHisAlaLeuAlaAspHisSerSerLeuAspArg----- 163
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

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QY 738 TGGAAAGATGGGTCCACTGCGCAGCTGTGTTGCGCTGAGACAACTTTTATATGCC 797
DB 164 ---SerSerGlyThrThrAlaLeuThrAlaLeuIleLeuThrAlaLeuIleAla 182
QY 798 AACCTCGAGATGTGTGGGCAATCTGTGTCGTTATATAGAGAGATCAAAACATGCA 857
DB 183 AaaAlaGlyAspSerArgAlaValLeu-----GlyValAspGlyArg 196
QY 858 GCCTTAAGCTTCAGCAAGACATTAATCCAACTCAGATGAGAGCGGATGAGATACAG 917
DB 197 AAlaIleGluLeuSerLysAspHisLysProAsnCyThrSerGluArgLeuArgIleGlu 216
QY 918 AAGCGTGAAGAAACGTCAAGGATGGCGGTGTTGGCGCTGCTAAGGTGCACGCTCC 977
DB 217 LysLeuGlyGlyValIleTyrAspGlyTyrLeuAsnGlyGluLeuSerValAlaArgAla 236
QY 978 ATTGGGAGCGGCGAGTACAG-----CGCGCGGTGTCACCTCTGTGCGCC 1022
DB 237 LeuGlyAspTrpHisIleLysGlyThrLysGlySerLeuCyProLeuSerCyValPro 256
QY 1023 GACATCAGACGCTGCGACGCTGACCCCAATGACAGGTTCAATTTTGGCGCTGTGAGG 1082
DB 257 GluLeuGluGluIleValLeuThrGluGluAspGluTyrLeuIleMetGlyCyAspGly 276
QY 1083 CTCTTCAAGGCTTTTACCCCAAGAAAGCCGTGAATCTTATCTTGTCTGTCTCGAGAT 1142
DB 277 LeuTrpAspValMetSerSerGlnCyValAlaValThrMetVal-----ArgArg 292
QY 1143 GAAAGATCCAGACCGGAGGAGAGATCCGACCGGACCGCGGCTTACGAAGACGCTGC 1202
DB 293 GluLeuMetGlnHisAsnAspProGluArgCyAspSerGlnAla----- 306
QY 1203 AACAGCTGCGCAACAGCGGTGTCAGCGGCTCGCGGACCAACGTCATGTGATGATG 1262
DB 307 -----LeuValLysGluAlaLeuGlnArgAsnSerCyAspAsnLeuThrValVal 324
QY 1263 GTG 1265
DB 325 Val 325

RESULT 13
H84643
Probable protein phosphatase 2C [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #ext_change 15-Jun-2001
C:Accession: H84643
R:Lin. X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayar, L.; Tallon, L.;
Euseb, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: H84643
A:Status: preliminary
A:Molecule type: DNA
A:Reads: 1-355 <STO>
A:Cross-References: GB:AE002093; NID:g4559345; PIDN:AAD23006.1; GSPDB:GNO0139
C:Genetics:
A:Gene: At2g25070
A:Map position: 2
C:Superfamily: human phosphoprotein phosphatase 1A

Alignment Scores:
Pred. No.: 1,166-19 Length: 355
Score: 353.50 Matches: 102
Percent Similarity: 44.398 Conservative: 64
Best Local Similarity: 27.274 Mismatches: 99
Query Match: 13.814 Indels: 109
DB: 2 Gaps: 13

US-09-935-124a-1 (1-1422) x H84643 (1-355)
QY 312 AAGACTGAAGGAGAAAGAGCAAAAGAGAAAACTCCGAGGAAAGAGAAATGGCACTGAA 371

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DB 9 LysThrGlu-----LysLeuSerGluAspGlyGluAsn----- 19
QY 372 GAGCTTGTGAAAAGAAAGTTTGTAAAGCCTCTTGATGATCTTGTGCTGAAGGCTAT 431
DB 20 -----AspLysLeuAspPheGlyLeu----- 26
QY 432 GTGGTGAACGGAGGTGAGAGGAGAGATGACAGATGCCACGTCATCTGAAAGAC 491
DB 27 ---SerSerMetGlnGlyTrpArgAlaThrMetGluAspAlaHisAlaAlaIleLeuSer 45
QY 492 ATCACCAGAGAGTGAAGGCCCATGTCCTCATTAATCTCGGGTTTCATATTTCGTG 551
DB 46 LeuAspAsp-----LysThrSerPhePheGlyVal 55
QY 552 TTGTATGACATGAGAGATTCGACCTCAAAATTTGTGTCAGCAATTTGATCAAAAC 611
DB 56 TyrAspGlyHisGlyGlyValValAlaLysPheCyValAlaLysTyrLeuHisGlnGln 75
QY 612 TTAATC-----AGAAAATTTCTTAAAGAGATGTATCATGTGATGAGAAAACGCTGAAG 665
DB 76 ValIleSerAsnGluAlaTyrLysThrGlyAsp-----ValGluThrSerLeuArg 92
QY 666 AGATGCCTT----- 674
DB 93 ArgAlaPhePheArgMetAspAspMetMetGlnGlyGlnArgGlyTyrPArgGluLeuAla 112
QY 675 -----TTGGACACTTTCAGACATCTGATGAAAGATTCCTT----- 710
DB 113 ValLeuGlyAspLysMetCAsnLysPheSerGlyMetIleGluGlyPheIleTrpSerPro 132
QY 711 -----AAACAAGCTTCCAGCCAGAACGCTGCTGG----- 740
DB 133 ArgSerGlyAspTrpHisAsnAsnGlnProAspSerTrpProLeuGluAspGlyProHisSer 152
QY 741 -----AAAGATGGGTCCACTGCGCACGTGTGTTGCTGCTGATGACAAACATT 785
DB 153 AspPheThrGlyProThrSerGlyCySerHisAlaCyValAlaLeuIleLysAspLysLys 172
QY 786 CTTTATATTTGCCAACCTCGGAGATAGTCGGGCAATCTGTGCGTTATATATAGAGAGT 845
DB 173 LeuPheValAlaAsnAlaGlyAspSerArgCyValIle-----Ser 186
QY 846 CAAAACATGTCAGCCTTAAAGCCTTCAGCAAGAGCATTAATCCAACTCAGATGAGAGCGG 905
DB 187 ArgLysSerGlnAlaTyrAsnLeuSerLysAspHisLysProAspLeuGluValGluLys 206
QY 906 ATGAGGATPACAGAGCGCTGAGAGAAACGTCAAGGATGGCGGTGTTGGCGCTGCTAGAG 965
DB 207 GluArgIleLeuLysAlaGlyGlyPheIleHisAlaGlyArgIleAsnGlySerLeuAsn 226
QY 966 GTGTCAAGCTCCATTTGGGAGCGGCGGAGTACAG-----CGC 1001
DB 227 LeuThrArgAlaIleGlyAspMetGluPheLysGlnAsnLysPheLeuProSerGluLys 246
QY 1002 TGGCGTGCACCTCTGTGTGCCGACATCAGACGCTCCAGCTGACCCCAATGACAGGTTTC 1061
DB 247 GlnMetValThrAlaAspProAspIleAsnThrIleAspLeuCyAspAspAspPhe 266
QY 1062 ATTTGTTGGCGCTGTGATGGGCTCTTCAAGGCTTTTACCCCAAGAAAGCCGTGAATTC 1121
DB 267 LeuValAlaLacCyAspGlyIleTrpAspCyMetSerSerGlnGluLeuValAspPhe 286
QY 1122 ATCTGTGCTGTCTGCAAGATGAAGAAATTCAGACCCGGGAAGGAAATCCGACACCGAC 1181
DB 287 IleHisGluGlnLeuLysSerLeu----- 294
QY 1182 GCCCGCTACGAAGACGCTGCAACAGCGTGGCCCAACAGCGGCTGACGCGGCTCGGCC 1241
DB 295 ThrLysLeuSerThrValCySerGluLysValValaAspArgCyLeuAlaLysProAspThrAla 314
QY 1242 -----GACACGTCACGTGATGTGTGTCGG 1268

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Db 315 ThrGlyGluGlyCysAspAsnMetThrIleIleValGln 328

RESULT 14

T04263

Phosphoprotein phosphatase (EC 3.1.3.16) ABI1 - Arabidopsis thaliana

N/Alternate names: protein F20B18.190

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999

C/Accession: T04263; A54588

R/Author: M.; Rose, M.; Hempel, S.; Entian, K.D.; Hohenseel, J.; Mewes, H.W.; Mayer, K.F.X

A/Reference number: Z15263

A/Accession: T04263

A/Molecule type: DNA

A/Residues: 1-434 <BMV>

A/Cross-references: EMBL:AL049483

A/Experimental source: cultivar Columbia; BAC clone F20B18

R/Meyer, K.; Leude, M.P.; Gfill, E.

Science 264, 1452-1455, 1994

A/Title: A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis th

A/Reference number: A54588; MUID:9425767; PMID:8197457

A/Accession: A54588

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-104, 'V', 106-434 <BMV>

A/Cross-references: GB:X78886; NID:9509418; PIDN:CAAS5484.1; PID:9509419

C/Genetics:

A/Map position: 4

A/Introns: 183/3; 280/3; 316/1

A/Note: F20B18.190

C/Keywords: phosphoric monoester hydrolase

Alignment Scores:

Pred. No.:	1,46e-19	Length:	434
Score:	352.50	Matches:	125
Percent Similarity:	44.71%	Conservative:	65
Best local Similarity:	29.41%	Mismatches:	148
Query Match:	13.77%	Indels:	97
DB:	2	Gaps:	19

US-09-935-124a-1 (1-1422) x T04263 (1-434)

QY 105 GACCTCTGGGGACCTTCGCGAGCCCGAGCGC--TCGCGCGCGCGCGCTCGCGGAGAA 161

Db 45 AspLeuMetValSerLeuProGluThrSerSerCysSerValSerGlySerHisGlySer 64

QY 162 GAAGCTCAGAAAGACCCCTGCTTTGATGATGATCTCCGCGCGAGCAGTACTGATCA 221

Db 65 GluSerArgIysValIleuIleSerArgIleAsnSerProAsnLeuAsnMetLysGluSer 84

QY 222 GATCAGGGGAGACCTTTCCTTTGATGATCTCCACCGCGTACGAGTGGCGAT----- 275

Db 85 AlaIleAlaAspIleValIleValIleAsp-----IleSerIleGlyAspGluIle 100

QY 276 TCAGTTCTCTGTCATCAATATCCAGATGATA--AAAGTGAAGGAGAAAGAGCA 332

Db 101 AenGlySerAspIleThrSerGluLysMetIleSerArgThrGlu----- 116

QY 333 AAGAGAAAACCTCCGAGAGAGAAAGATGCGATGAGAAAGCTTGTCGAAAAGATT 392

Db 117 -----SetArgSerLeuPheGluPheLys--- 124

QY 393 TGTAAAGCTCTTCGTCATCTTTGTCCTAAGGCTATGTGCGAGCGAGCGTGAAG 452

Db 125 -----SerValProLeuArgIlePheThrSerIleCys-----GlyArg 137

QY 453 AGGAGAGATGACGATGCGCAGCTGATCTTGAACGATCAACGAGAGAGTGAAGCCC 512

Db 138 ArgProGluMetGluAspAla-----ValSerThrIleProArgPheLeuGlnSer 154

QY 513 CCAATGCTCCATTT-----ACTGGGTTTCAATATTTTGCT 548

Db 155 SerSerGlySerMetLeuAspGlyArgPheAspProGlnSerAlaIlePheAspGly 174

QY 549 GTTTTGTGATGACATGAGAGAAATTCGAGCCCTCAAAAATTGCTGACAGAAATTCATCA 608

Db 175 ValIysAspGlyHisGlyGlySerGlnValAlaAsnIleCysArgIleArgMetHisLeu 194

QY 609 AACTTATTCAGAAAATTTCTTAAA-----GGAGATGTAATCAGT 647

Db 195 AlaLeuIleGluIleIleAlaIleGlySerProMetLeuCysAspGlyAspThr---Trp 213

QY 648 GTACAGAAAACCGTAGAGATGCGCTTTTGACACTTTCAGAGATCTGATGAGAGATTC 707

Db 214 LeuGluIysTrp---LysIleValAlaLeuPheAsnSerPheLeuArgValAspSerGluIle 232

QY 708 CTTAAACAGCTTCACCGCAGAGAGCTGCTCGAAGAGGGGTGACCTGCGACGTTGT 767

Db 233 GluSerValAlaProGluThrVal-----GlySerHisSerValAla 247

QY 768 CTGCGCTGACAGCAATCTTTATATATGTCACCTCGAGATATGTCGGCATCTGTGT 827

Db 248 ValAlaPheProSerHisIlePheValAlaAsnIleCysArgIleValAlaLeuGly 267

QY 828 CATTATATAGAGAGAGTCAAAAACATGACAGCTTAAAGCTTCAGCAAGAGCATATATCA 887

Db 268 Arg-----GlyLysThrAlaLeuProLeuSerValAspHisLysPro 281

QY 888 ACTCAGATATAGAGCGGATGAGATACAGAGAGCTGAGAGAAACGTC-----AGG 938

Db 282 AspArgGluAspGluAlaIleArgIleGluIleAlaIleGlyGlyLysValIleGlnTrpAsn 301

QY 939 GATGGCGGTGTTTGGCGCTGATGAGGTGTCAGCGCTCATCTTGGAGCGGAGTACAG 998

Db 302 GlyAlaArgValPheGlyValIleuIleMetSerArgSerIleGlyAsp---ArgIleu 320

QY 999 CGCTGGCGGTGTCACCTGTCGCGCATGACAGCGTGCAGCGTGCAGCCGAGTCAACAG 1058

Db 321 LysProSerIleIleProAspProGluValIleAlaValArgValIleGluAsp 340

QY 1059 TTCAATTTTGTCGCTGTAAGGCTCTTCAAGCTTTTACCCGAGAAAGCGTGAAC 1118

Db 341 CysLeuIleLeuAlaSerAspGlyValIleTrpAspValIleMetIleAspGluIleGly 360

QY 1119 TTCATC-----TGTGCC 1130

Db 361 MetAlaArgLysArgIleLeuLeuTrpHisLysAsnAlaValAlaGlyAspAlaSer 380

QY 1131 TGTCTGAGGATGAAAGATCCAGACCGGAGAGAGAGTCCGACCGCGCTAC 1190

Db 381 LeuLeuAlaAspGluArg-----ArgLysGluIleLys-----AspProAlaIle 395

QY 1191 GAACGACCTGCAACAGGCTGCGCAACAGCGGCTGACGCGGCTGCGCCAGCAACGTC 1250

Db 396 MetSerAlaIleGluTrpLeuSerIleLeuAlaIleGlnArgIleSerLysAspAsnIle 415

QY 1251 ACTGTATGGTGGTG 1265

Db 416 SerValValValVal 420

RESULT 15

F84650

Probable protein phosphatase 2C (imported) - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 01-Mar-2002

C/Accession: F84650

R/Klin, X.; Kaul, S.; Rounleley, S.D.; Shee, T.P.; Benito, M.I.; Town, C.D.; Fujita, C.Y.;

M.; Koo, H.; Morfitt, K.S.; Cronin, L.A.; Shen, M.; Yankem, S.E.; Umayam, L.; Tallon, L.;

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: AB4420; MUID:20083487; PMID:1067197

A/Accession: F84650

A/Status: preliminary

A/Molecule type: DNA


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Db 90 -LeuSerIleProValAla-----ProValGlyIleAlaAlaProIleSerAenAl 106
QY 248 TGAATCCCAACCCGCTAGCAGTGCATTCAGTTCTCTTGCCACATCAATATCCAGAT 307
Db 106 AaerThrProArgGlu-----SerArgAl 115
QY 308 GGTAAAGACTGAAGGAAAGCAAGAGAAAAACCTCCGAGAAAGAAATGGCAG 367
Db 115 aValGluArgGluGlyAerGly----- 122
QY 368 TGAAGACTTGGAAGAAAGTTTAAAGCTTTGGGATCTTGGTCTGAAGG 427
Db 123 -----TyrSerValTyrCybLys----- 128
QY 428 CTATGTGCTGAGCGAAAGGTGAGAGGAGAGATGCAGATGCCACGTATCTGAA 487
Db 129 -----ArgGlyLysArgGluAlaMetGluAerPargPheSerAlaIleTh 143
QY 488 CGACATCACGAGAGTGTAGGCCCCCATGTCCTCATTACTCGGCTTCATATTTGC 547
Db 143 rAenLeuGlnGlyAer-----ProLysGlnAlaIle-----PheG1 155
QY 548 TGTTTTGAATGACATGAGAGAAATTCAGGCTCAAAATTTGCTGCACAGATTTGCATCA 607
Db 155 yValTyrAerGlyHisGlyGlyProThrAlaAlaGluPheAlaIalysAenLeuCyse 175
QY 608 AAATCTTAATCAGAAATTTCTTAAAGAGATGTATC-----AGTGT 649
Db 175 rAenIleLeu-----GlyGluIleValGlyArgAenGluSerLysI1 190
QY 650 AGAGAAACCGTGAAAGAGATGCTTTTGACACTTTCAGCACTTACAGCACTTGTAAAGTCTCT 709
Db 190 eGluGluAlaValLysArgGlyLysLeu-----AlaThrAerSerGluPheLe 206
QY 710 TAAACAGAGCTTCAGCCAGAAAGCTGCTGAAAGATGGGTCTCACTGCCAGCTGTGCTT 769
Db 206 uLysGluLysAenVal-----LysGlyLysSerCybValThrAlaLe 221
QY 770 GCGCTGACGAAATCTTTATATTCGCAACTCGAGATAGTGGGCAATCTTGTCG 829
Db 221 uIleSerAerPglAenLeuValValAlaAenAlaGlyAerCybArgAlaValLeu----- 239
QY 830 TTATTAATGAGAGAGCTCAAAAACATGACGCTTAAAGCTTCAGCAAGAGCATATATCCAC 889
Db 240 -----SerValGlyGlyPheAlaGluAlaLeuThrSerAerPglAerProSe 255
QY 890 TCAGTATGAAGAGCGATGAGATACAGAAAGCT----- 923
Db 255 rArgAerAerPglAerAenArgIleGluSerSerValArgIleLeuAlaLysGluValTh 275
QY 924 -----GGAGGAAACGT 934
Db 275 rValArgPheTyrHisAerPyrMetValLeuIleThrIleIleLeuGlnGlyLysYrVa 295
QY 935 CAGGAGT-----GGGCGTGTGTTGGCGCGCTGAGAGGTGCACAGCTCCATGG 982
Db 295 laerThrPheAenSerValITrPArgIleGlnGlySerIleValAlaSerArgGlyIleG1 315
QY 983 GGAACGGGACGTACAGCGCGCTGCGCTGCTGCGCCGACATCAGACGCTGCCAGCT 1042
Db 315 yAerAlaHisIleLeuLysGln---TrpIleIleSerGluProGluIleAenIleLeuArgI1 334
QY 1043 GACCCCAATGACAGCTTATTTGCTGCTGATGGGCTCTTCAAGGCTTTAAACCC 1102
Db 334 eAenProGlnHisGluPheLeuIleLeuAlaSerAerPglLeuTrpAerLysValSerA 354
QY 1103 AGAAGAAAGCTGAATTCATCTTGCTCTCTCGAGATGAAGAAAGATCCAGACCCGGA 1162
Db 354 ngInGluAlaValAerIle-----AlaArgP 363
QY 1163 AGGAGATGCCGAGCCGACCGCTACGAA-----GCAGCTTCAGACAGGCTGCGCA 1216
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Db 363 oPheCyLeGlyThrAerGlnLysArgLysProLeuLeuAlaCybLysLeuValA 383
QY 1217 CAAGCGGTGCACAGCGGCTGCGCCGACAGCTGATGATGATGATGCGGATGAGGCA 1276
Db 383 pleuSerValSerArgGlySerLeuAerAerPglIleSerValMetLeuIleGlnLeuCybH1 403
QY 1277 C 1277
Db 403 s 403

RESULT 17
106308
protein phosphatase 2C homolog F11C18.60 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001
C/Accession: T06308
R/Beyan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.; De
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1999
A/Reference number: Z15589
A/Accession: T06308
A/Molecule type: DNA
A/Residues: 1-357 <BEV>
A/Cross-references: EMBL:AL049607; GSPDB:GN00062; ATSP:F11C18.60
A/Experimental source: cultivar Columbia; BAC clone F11C18
C/Genetics:
A/Gene: ATSP:F11C18.60
A/Map position: 4
A/Introns: 39/3; 61/1; 97/2; 148/3; 190/3; 232/1; 257/3; 275/2; 293/3
C/Superfamily: human phosphoprotein phosphatase 1A

Alignment Scores:
Pred. No.: 2,196-19 Length: 357
Score: 350.00 Matches: 95
Percent Similarity: 46.25% Conservative: 52
Best Local Similarity: 26.35% Mismatches: 85
Query Match: 13.67% Indels: 64
DB: 2 Gaps: 11

US-09-935-124a-1 (1-1422) x T06308 (1-357)
QY 432 GTGCGTGAAGCGAAGGTGAGAGAGAGAGATGAGATGCCAGTCACTGTAAGCAC 491
Db 432 ----- 45
QY 492 ATCACCGAGAGGTGTAGGCGCCCATGCTCCCTCATTACTCGGCTTTCATATTTGCTGTT 551
Db 492 -----AsnThrSerPheLeuGlyVal 55
QY 552 TTGATGATGAGAGAAATTCAGAGCTCAAAATTTGCTGCACAGAAATTTGCATGAAC 611
Db 552 ----- 75
QY 612 TTATTC-----AGAAATTTCTTAAAGAGAGATGTA---ATCGGTGTAGAGAAACGCTG 662
Db 612 ----- 95
QY 663 AAGAGATGCTTTTGACACTTTCAGAGATGTCAGTGAAGAGTCTTAAACAGCT--- 719
Db 663 -----MetAerGluMetGlnGlyGlnArgGlyITrPArgIleLeuAlaVal 113
QY 719 ----- 719
Db 719 ----- 133
QY 720 -----TCCAGCCGAAGCT---GCCTGG----- 740
Db 720 ----- 153
QY 741 -----AAAGATGGGTCCACTGCGCACGTTGTTCTGCGCTGTGAGACATTTCTT 788
Db 741 ----- 173
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Db      124  GUGUAAP----- 126
|||:|:|:
408  GTGATCTTTGCTGAAGGCTAT-----GTGCTGAGCGGAAGGTGAGAGAGAG 461
|||:|:|:
Db      127  -----GlyTyrTyrSerValTyrCylsValargIylargGlyPro 140
|||:|:|:
462  ATGACAGATGCCACGTCATCTGAAAGACATCAGACGAGAGGTGAGGCCCATGCTCC 521
|||:|:|:
Db      141  MetGluAspArgTyrPheAlaAlaValAspArgAsnAspArgIylGly----- 156
|||:|:|:
522  CTCATTAATCTGGGTTTCATATTTTGTCTTTTGTGAGACATGAGAAATTCAGGCTCA 581
|||:|:|:
Db      157  -----TyrTysAsnAlaPhePheGlyValPheAspGlyHisGlySerIylAla 174
|||:|:|:
582  AAATTTGCTGCAGACAGATTGTCATCAAACTTAATCAGAAAATTCTTAAGA----- 635
|||:|:|:
Db      175  GUGPheAlaAlaMetAsnLeuGlyAsnAsnIleGluAlaAlaMetAlaSerAlaArgSer 194
|||:|:|:
636  -----GATGTAACTAGGTAGAGAAAACCGTAGAAGATGCTTTTGCACCTTTCAG 689
|||:|:|:
Db      195  GlyGluAspGlyCysSerMetGluSerAlaIleArg-----GluGlyTyrIle 210
|||:|:|:
690  CATACTGATGAAGAGTTTCTTAACAAGCTTCAGCCAGAACGCTGCGGAAGATGG 749
|||:|:|:
Db      211  LysThrAspGluAspPheLeuLysGluGlySer-----ArgGlyGly 224
|||:|:|:
750  TCCATGCGCCACGTGTGCTGTGCTGTAGACAACATTTTATATGCAACTCGGAGAT 809
|||:|:|:
Db      225  AlaCysCysValThrAlaLeuIleSerLysGlyGluLeuAlaValSerAsnAlaGlyAsp 244
|||:|:|:
810  AGTGGGCAATCTTGTGTGCTTAAATGAGAGAGTCMAAAACATCAGCTTAAGCTTC 869
|||:|:|:
Db      245  CysArgAlaValMet-----SerArgGlyGlyThrAlaGluAlaLeu 258
|||:|:|:
870  AGCAAGAGCATTAATCCAACTGATGAGAGCGGATGAGATACAGAAAGCTGAGAG 929
|||:|:|:
Db      259  ThrSerAspHisAsnProSerGlnAlaAsnGluLeuLysArgIleGluAlaLeuGlyGly 278
|||:|:|:
930  AACGTGAG-----GATGG-----CGTTTGGGCGCTGTAGAGGTGTCAGCTCC 977
|||:|:|:
Db      279  TyrValAspCysCysAsnGlyValIleTrpArgIleGlnGlyThrLeuAlaValSerHisGly 298
|||:|:|:
978  ATTGGGAGCGGCGAGTACAAAGCGCTCGGTGTCACCTGTGTGCGCCAGATCAGACGCTGC 1037
|||:|:|:
Db      299  IleGlyAsp---ArgTyrLeuLysGluTrpValIleAlaGluProGluThrArgThrLeu 317
|||:|:|:
1038  CAGCTACCCCAATGACAGGTTCAATTTGTTGGCTGTGATGGGCTTTCAAGGTCCTTT 1097
|||:|:|:
Db      318  ArgIleLysProGluPheGluPheLeuIleLeuAlaSerAspIleLeuTrpAspLysVal 337
|||:|:|:
1098  ACCCGAAGAAAGCGGTGAACCTTACTGTTGTC-----TGTCTGAGAGTAAAGATCCAG 1154
|||:|:|:
Db      338  ThrAsnGlnGluAlaValAspValIleArgProTyrCysValGlyValGluAsnProMet 357
|||:|:|:
1155  ACCCGGAAAGGAAGTCCCGACGCCGCGCTAGAGAACAGCTGCAACAGGCTGACC 1214
|||:|:|:
Db      358  ThrLeu-----SerIleCysLysLysLeuAla 366
|||:|:|:
1215  AACAGGCGGTGACGCGGCTGCGCCGACACGTCATGTGATGTGTGCGGATCA 1271
|||:|:|:
Db      367  GluLeuSerValLysArgLysSerLeuAspAspIleSerLeuIleIleGlnLeu 385
|||:|:|:
RESULT 21
S22422
phosphoprotein phosphatase (BC 3.1.3.16) 1A-alpha - rabbit
NAlternate names: magnesium-dependent protein phosphatase 1A; protein serine/threonine
CSpecies: Oryctolagus cuniculus (domestic rabbit)
CDate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #ext_change 15-Jun-2001
CAccession: S22422
RManu: D.J.; Campbell, D.G.; McGowan, C.H.; Cohen, P.T.W.
Biochim. Biophys. Acta 1130, 100-104, 1992
ATitle: Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and comparative

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A.Reference number: S22422; MUID:92182001; PMID:1311954
A.Accession: S22422
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-382 <MAN>
A.Cross-references: GB:S8757; NID:G247166; PID:AA821783.1; PID:G247167
C.Superfamily: human phosphoprotein phosphatase 1A
C.Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Alignment Scores:
Pred. No.: 1,366-18 Length: 382
Score: 340.00 Matches: 101
Percent Similarity: 49.33% Conservative: 47
Best Local Similarity: 33.67% Mismatches: 104
Query Match: 13.28% Indels: 48
DB: 2 Gaps: 12

US-09-935-124a-1 (1-1422) x S22422 (1-382)

QY      417  GGTGTGAAGGGCTATGTGGCTGAGCGGAAGGTGAGAGAGATGACAGATGCCAC 476
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Db      21  GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTrpArgValGluMetGluAspAlaHis 40
|||:|:|:
QY      477  GTTATCTGACGACATACCGAGAGGTGTAGGCCCCCATGCTCCCTCATTACTGGGTT 536
|||:|:|:
Db      41  ThrAlaValIleGlyLeu-----ProserGlyLeuGluThr---Trp 53
|||:|:|:
537  TCAATATTTTGTGCTTTTATGATGACATGAGAGATTCGAGCTCAAAATTTGCTGACAG 596
|||:|:|:
Db      54  SerPhePheAlaValTyrAspGlyHisAlaGlySerGlnValAlaLysTyrCysGlu 73
|||:|:|:
QY      597  AATTTGACATCAAACTTAATCAGAAAATTTCTCT---AAAGAGAT-----GTAACTAGT 647
|||:|:|:
Db      74  HisLeuLeuAspHisIleThrAsnAsnGlnAspPheLysGlySerAlaGlyAlaProser 93
|||:|:|:
QY      648  GTAGAGAAAACCGTAGAGATGCTTTTGCACCTTTCAGACATCTGATGAAGATTC 707
|||:|:|:
Db      94  ValGlu---AsnValLysAsnGlyLeuArgThrGlyPheLeuGluIleAspGlnHisMet 112
|||:|:|:
708  CTTAACAAGCTTCGACGCGAGAGCGCTCGCTGGAAGATGGGTGTCAGCTGCGTGT 767
|||:|:|:
Db      113  ArgValMetSerGlnLysValHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
|||:|:|:
768  CTGCGCTGTAGACACATCTTATATGTCSCAATCTCGAGATAGTCGGGCAATCTTGTGT 827
|||:|:|:
Db      133  LeuIleSerProGlnHisThrTyrPheIleAsnGlySerGlyAspSerArgGlyLeuLeuGly 152
|||:|:|:
QY      828  CGTTATTAATGACAGAGATCAAAACATGACGCTTAAGCTTACGAAAGCATTAATCCA 887
|||:|:|:
Db      153  Arg-----AsnArgLysValHisPhePheThrGlnAspHisLysPro 166
|||:|:|:
QY      888  ACTCAGTATGAAGAGCGGATGAGATGACAGAAAGCTGAGAGAAAGTCAGAGATGGGCT 947
|||:|:|:
Db      167  SerAsnProLeuGlnLysGluArgIleGlnAsnAlaGlyLysSerValMetIleGlnArg 186
|||:|:|:
QY      948  GTTTTGGCGCTGTAGAGGTGTACGCTTCATTTGGGAGCGGCGACATACAGCGCTGC--- 1004
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Db      187  ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTyrLys---CysVal 205
|||:|:|:
QY      1005  -----GGTGTACC-----TTGTGCCGACATCAGA 1031
|||:|:|:
Db      206  HisGlyLysGlyProThrGlnGlnLeuValSerProGluProGluValHisAspIleGlu 225
|||:|:|:
QY      1032  CGCTGCCAGCTGACCCCAATGACAGTTCATTTTGTGGCTGAGAGGCTCTTCAAG 1091
|||:|:|:
Db      226  ArgSerGlu-----GluAspAspGlnPheIleIleLeuAlaCysAspGlyIleTrpAsp 243
|||:|:|:
QY      1092  GTCTTACCCCAAGAGAGAGCGGTGACATTCCTGCTGCTGTGAG-----GATGAA 1145
|||:|:|:
Db      244  ValMetGlyAsnGlnGlnLeuCysAspPheValaArgSerArgLeuGlnValThrAspAsp 263
|||:|:|:
QY      1146  AAGATTCAGACCCGGGAAAGGAAGTCCGACGCCGCGCTAGAGAACAGCTTGACAC 1205
|||:|:|:

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Db 264 -----LeuGluYsValCyAsn 269

Qy 1206 AGCGTGGCCAAAGCGGCTGCGGCCGACAAAGTACCTGAGTGGCG 1265
Db 270 GluValValAspThrCyLeuTrpYLeuGlySerArgAspAsmMetSerValIleLeuIle 289

RESULT 22

A32399
phosphoprotein phosphatase (EC 3.1.3.16) 1A - rat
N/Alternate names: protein phosphatase 2C
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Jul-1989 #sequence_rev15101-0ul-1989 #text_change 15-Jun-2001
C/Accession: A32399
R/Tamura, S.; Lynch, K.R.; Larner, J.; Fox, J.; Yasui, A.; Kikuchi, K.; Suzuki, Y.; Tsui
Proc. Natl. Acad. Sci. U.S.A. 86, 1796-1800, 1989
A/Title: Molecular cloning of rat type 2C (1A) protein phosphatase mRNA.
A/Reference number: A32399; MUID:89184515; PMID:2538815
A/Accession: A32399
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-382 <TAM>
A/Cross-references: GB:J04503; NID:9206312; PID:AAA41917.1; PID:9206313
C/Keyword: liver; phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Alignment Scores:

Pred. No.:	1,36e-18	Length:	382
Score:	340.00	Matches:	101
Percent Similarity:	49.33%	Conservative:	47
Best Local Similarity:	33.67%	Mismatches:	104
Query Match:	13.28%	Indels:	48
DB:	2	Gaps:	12

US-09-935-124A-1 (1-1422) x A32399 (1-382)

Qy 417 GGTCTGAAGGCTATGTGCTGACGCGAGGAGAGAGATGCAAGTCCAC 476
Db 21 GlyLeuArgTrpGlyLeuSerSerMetGlnGlyTPrArgValGluMetGluAspAlaHis 40

Qy 477 GTATCTCTGAACGATCATCAGGAGAGTGAAGCCCATCGCTCATATACCTGGGTT 536
Db 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGlnThr---Trp 53

Qy 537 TCATATTTTGGCTTTTGGATGACATGAGAGATTCGAGGCTCAAAATTTGCTGCACAG 596
Db 54 SerPhePheAlaValTrpArgLysIleAlaGlySerGlnValAlaLeuTrpCywGlyVal 73

Qy 597 AATTTCGATCAAACTTAATCAAAAATTTCCT--AAAGCAT-----GTATACGT 647
Db 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheLeuGlySerAlaGlyAlaProSer 93

Qy 648 GTAGAGAAAACCTGAAGAGATGCTTTTGGACATTTTCAAGCATATGATGAAGATT 707
Db 94 ValGlu--AsnValValAsnGlyIleArgThrGlyPheLeuGluIleAspGlnHisMet 112

Qy 708 CTTAAACAGCTTCCAGCCAGAACGCTGCTGGAAGATGGTCCATGCTCCACGTGTGT 767
Db 113 ArgValMetSerGluLeuGlnIleGlyAlaAspArgSerGlySerThrAlaValGlyVal 132

Qy 768 CTGGGTGTAGACACATCTTTATATGTCGCACTGCGAGATGATGGCGGACATCTGTGT 827
Db 133 LeuIleSerProGlnIleThrTrpPheIleAsnCyGlyAspSerArgGlyLeuLeuCyw 152

Qy 828 CGTTATATGAGAGAGATCAAAACATGACGCTTAAAGCTGACGAAAGACATTAATCCA 887
Db 153 Arg-----AsnArgValAlaHisPhePheThrGlnAspHisIlePro 166

Qy 888 ACTCAGATGAGAGCGAGATGAGATGACAGAGCTGAGAGAAAGTCCAGGATGGGCGT 947
Db 167 SerAsnProLeuGlnIleGluArgIleAsnAlaGlyLeuGlySerValMetIleGlnArg 186

Qy 948 GTTTTGGCGCTGTAGAGGTTCACGCTCCATTTGGGACCGGACATACACGCTGC-- 1004
Db 167 SerAsnProLeuGlnIleGluArgIleAsnAlaGlyLeuGlySerValMetIleGlnArg 186

Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTrpTrp---CywVal 205

Qy 1005 -----GRTTCACC-----TCTGTCCCGGACATCGA 1031
Db 206 HisGlyLeuGlyProThrGlnLeuValSerProGluProGluValHisAspIleGlu 225

Qy 1032 CGCTGCCAGCTGACCCCAATGACAGGTTCAATTTGTGGCTGTGAGTGGCTCTTCAAG 1091
Db 226 ArgSerLeu-----GluAspAspGlnPheIleIleLeuAlaCywAspLysIleTrpAsp 243

Qy 1092 GTCTTATCCCAAGAGAGACCCGTGAATCTTCAATCTTGTCTGTCTGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGlnIleLeuCywAspPheValArgSerArgLeuGlnValThrAspAsp 263

Qy 1146 AAGATCCAGACCCGAGAGAGAAATCCGACCCGCTACGAGCAGCTGCAAC 1205
Db 264 -----LeuGlnIleValCywAsn 269

Qy 1206 AGCGTGGCCAAAGCGGCTGCGGCCGACAAAGTACCTGAGTGGCG 1265
Db 270 GluValValAspThrCyLeuTrpYLeuGlySerArgAspAsmMetSerValIleLeuIle 289

RESULT 23

T48018
hypothetical protein T17013.220 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 20-Apr-2000 #sequence_rev15101-0ul-2000 #text_change 20-Apr-2000
C/Accession: T48018
R/Rieger, M.; Mueller-Auer, S.; Zilp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, February 2000
A/Reference number: Z24482
A/Accession: T48018
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-383 <RIE>
A/Cross-references: EMBL:AL138651
A/Experimental source: cultivar Columbia; BAC clone T17013
C/Genetics:
A/Map position: 3
A/Introns: 56/3; 118/3; 197/2
A/Note: T17013.220

Alignment Scores:

Pred. No.:	1,78e-18	Length:	383
Score:	338.50	Matches:	108
Percent Similarity:	45.57%	Conservative:	67
Best Local Similarity:	28.12%	Mismatches:	128
Query Match:	13.22%	Indels:	81
DB:	2	Gaps:	15

US-09-935-124A-1 (1-1422) x T48018 (1-383)

Qy 183 CTCTTGTAGTACCTCCCTCGGCGACAGTACTGATCAGATCAGGGGACCTTTGCTT 242
Db 21 LeuPheAspGlyVal-----SerSerAlaValLysSerProValSerSerProLysLeu 38

Qy 243 TTTGATGATCTCCACCCGCTAGCAGTGGCGGATGACAGTTCTTGTCCACATCATATCC 302
Db 39 -----GlyPheThrGlnSerThrAlaSerValSerLysSerLeuThrThrSerProVal 56

Qy 303 CAGATGTAAGACTAAAGCTAAAGAGAAAGCAAAAGAAAACCTCCGAGAAAGAAAGAT 362
Db 57 AlaAspIlePheProGlnIleLysP----- 64

Qy 363 GGCAGTAAAGCTTGTGAGAAAGAAAGTTGTAAAGCTCTTGGTATCTTTGGTGTG 422
Db 65 -----CysAspProSer-----Val 69

Qy 423 AAGGCTATGTGGCTAGCGGAG-----GTCAGAGGAGAGAG 461
Db 70 LeuAspTrpIleProThrIleArgSerGlySerPheAlaAspIleGlyProLysArgAsn 89

Qy 462 ATGAGAGATGCCAGCTCATCTTGAACGACATCACGAGGAGTGTAGCCCCCATGCTCC 521

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RESULT 1
P2C_PARTE
ID_P2C_PARTE      STANDARD;      PRT;      300 AA.
AC      P49444;
DT      01-FEB-1996 (Rel. 33, Created)
DT      01-FEB-1996 (Rel. 33, Last sequence update)
DT      01-NOV-1997 (Rel. 35, Last annotation update)
DE      Protein phosphatase 2C (EC 3.1.3.16) (PP2C).
OS      Paramoecium tetraurelia.
OC      Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Pencilula;
OC      Paramoecium
OC      NCBI_TaxID=5886;
RN      [1]
RP      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC      SPRAIN-SIS.
RX      MEDLINE#95105156; PubMed#7866499;
RA      Klump, S., Hanke, C., Donella-Dearna A., Beyer A., Kellner R.,
RA      Pina L.A., Schultz U.B.
RT      A membrane-bound protein phosphatase type 2C from Paramoecium
RT      tetraurelia. Purification, characterization, and cloning."
RL      J. Biol. Chem. 269:32774-32801(1994).
CC      -1 FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC      -1 CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC      phosphate.
CC      -1 COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC      -1 SUBCELLULAR LOCATION: Membrane-bound.
CC      -1 PTM: THE N-TERMINUS IS BLOCKED.
CC      -1 SIMILARITY: BELONGS TO THE PP2C FAMILY.
-----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      or send an email to license@sb-sib.ch).

```


CC	phosphate.
CC	-1- COPOLYMER: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY) .
CC	-1- SUBUNIT: MONOMER.
CC	-1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; L34882; AAA6732.1; -
DR	EMBL; Z54354; CAA91172.1; -
DR	HSSP; P35813; 1A6O.
DR	InterPro; IPR001932; PP2C-1like.
DR	InterPro; IPR002222; PP2C.
DR	Pfam; PF00481; PP2C; 1.
DR	SMART; SMO0331; PP2C_SIG; 1.
DR	SMART; SMO0333; PP2CG; 1.
DR	PROSITE; PS01032; PP2C; 1.
FM	Hydrolase; Magnesium; Manganese; Multigene family.
FT	METAL 37
FT	METAL 38
FT	METAL 62
FT	METAL 230
FT	METAL 279
FT	CONFLICT 196
FO	SEQUENCE 414 AA; 44856 MW; EF03A16625A2B11 CRC64; K -> T (IN REF. 1).
	MANGANESE 1 (BY SIMILARITY)
	MANGANESE 1 (BY SIMILARITY)
	MANGANESE 1 AND 2 (BY SIMILARITY) .
	MANGANESE 2 (BY SIMILARITY)
	MANGANESE 2 (BY SIMILARITY) .
	MANGANESE 2 (BY SIMILARITY) .
	K -> T (IN REF. 1) .

Alignment Scores:

Pred. No.:	6,7e-20	Length:	414
Score:	380.50	Matches:	111
Percent Similarity:	48.54%	Conservative:	55
Best Local Similarity:	32.44%	Mismatches:	105
Query Match:	14.86%	Indels:	71
DB:	1	Gaps:	14

US-09-935-124A-1 (1-1422) x P2C3_SCHPO (1-414)

Oy	342	ACCTCCGAGGAAAGAAAGAAATGGCAGTGAAGACCTTGTGAAAGAAAGAAAGTTTGAAGACC	401
Db	10	ThhGluysHsisserValhenglSerhengluph-----	21
Oy	402	TCCTTCGGATCTTGGCTGTGAAGGGCTAATGTGCTGACCGAAGGGGTGAAGAGGAG	461
Db	22	-----ValleuTryglLeu-----SerSerMetgingllyTryphglleSer	35
Oy	462	ATGCAAGATGGCCACGTCACTCTGAAAGCATCAACGAGATGATGAGCCCCCACTGCC	521
Db	36	Metgluaprahahiserialale-----LeuSerMetGluys-----Serla	50
Oy	522	CTCATTAATCGGGTTTCATATTTCCTGTTTGAATGACATGACGAATTCGACCTCA	581
Db	51	VallyrAspProvalaAspPhehPhehAlaValyAspPolylhAsglYAlaPlyValAla	70
Oy	582	AAATTTCGTGCACGAATTTGCATGAACCTTAATACAGAAA-----TTTCTTAAGCA	635
Db	71	lyrTrpCyAsglYSerheneuProglInlleuGluYAsmProAspPheglInlySgl	90
Oy	636	GATGTAATCAAGTGTAGAGAAAAC-----GTGAGAGATGCTCTTTTGGACACT	683
Db	91	AspPheValhahnaIaleuYsserSerPheleuAsnAlaAspYValaIleleuAsp---	109
Oy	684	TTTCAGCATACTGTATGAGAGGTTCTTAAACAAGCTTCACGCCAAGAGCTGCTGGAAA	743
Db	110	-----AspAspGlnPhehIsthAspProSer-----	118
Oy	744	GATGGTCACATCGACAGCTGTGTCTTGGCTGTGTAGACAACTTTATTTATTCGAACCTC	803
Db	119	-----GlyCySerhIalathrValValleuYrValGlyAsnYlYsleuYrCyValaIasnhla	137

Dy		804	GAGGATAGTCGGCGCAAACTTGTCTGTTATATGAGAGAGTCAAACCATGACGGCTTA	863
Dy		138	gIyApsrArghTrvAlleu-----glySerlyegIyleAlTyS	151
Dy		864	AGCCTCAGAAAGGCATTATCCACTCAGTATGAAGAGCGGAGATACAGAAAGGCT	923
Dy		152	ProteinSerAlaaphSIyPProSerAnGIuAlGIuYSAIArGlIeCySAIAIA	171
Oy		924	GGAGGAAAACGTACAGGATATGGCGCTGTTTTGGCGCTGTACAGGCTCACGCTCCATGGG	983
Dy		172	gLyglYpHevalAapHeelgYArGVAlaenGIyaenLIaLeuaIaleSeRrAgAlleGIy	191
Oy		984	GAGCGGACGTACAAAGCCGTCGGT-----GTCACTCTGTGTGCC	1022
Dy		192	AapHeGluPluPeLyAanSerAenLeuGIuPogIuYsgInIIeValThrAlaLeuPo	211
Oy		1023	GACATACAGACGCTCCACGCTGACCCCCCAATACAGATTCATTTTGTTGGCTGTGATGG	1082
Dy		212	AspValValValHISguIlleThraPaPaPaPaGIuPeVaIVAlleuaIaCySaPaBgIy	231
Oy		1083	CTCTTCAGATCTTTAACCCCGAAGAAGCCGTGAACCTTCATCTTGTCCTGTCTCAGAGAT	1142
Dy		232	IletPaPaCySlYbThrsErGIuGIuValIIleGIuPeVal-----	245
Oy		1143	GAAGAATCTCAGACC CGGAAGGAGAGTCCGCAGCCGACGCGCGCTACAGACAGCC--	1199
Dy		246	-----ATgaTgGIyIIeValAIaGIyThrsleuGIuYsIIeAlaGIu	260
Oy		1200	-----TGCAACAGGCTGTGGCCAAACAAGGCGTGCAGCGGGCG--TCGGCCGCAAC	1247
Dy		261	AenLeuMeLApAaPhaNCysIIeAlaIsErAepThrgIuThrHgIyeuGIySAaPaPhn	280
Oy		1248	GTCACTGTGATGTGTGTGCGGATAGGGCATGAGGGGTGGCGCGGCCGACAGACAGCA	1307
Dy		281	MethThraValCySlIeValAlaLeu-----LeuGIuGIuAaenAplySSerAla	296
Oy		1308	TGGTAT	1313
Dy		297	TriTYr	298
RESULT 3				
P2C2_SCHPO				
ID	P2C2_SCHPO	STANDARD;	PRT;	370 AA.
AC	Q09172;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).			
GN	PFIC2 OR SPIC2123.11.			
OS	Schizosaccharomyces pombe (fission yeast).			
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;			
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;			
OC	Schizosaccharomyces.			
OX	NCBI_TaxID=4896;			
NP	SEQUENCE FROM N.A.			
RP				
RC	STRAIN=972;			
RC	MEDLINE=95163582; PubMed=7859738;			
RA	Shiozaki K, Russell P,			
RA	"Counteractive roles of protein phosphatase 2C (PP2C) and a MAP			
RT	kinase homolog in the osmoregulation of fission yeast.",			
RL	EMBO J. 14:492-502(1995).			
RN				
RE	SEQUENCE FROM N.A.			
RF	STRAIN=972;			
RC	MEDLINE=21849401; PubMed=11859360;			
RA	Wood V., Gillilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,			
RA	Scouras J., Peat N., Hayles J., Baker S., Baeham D., Bowman S.,			
RA	Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,			
RA	Collins M., Connor R., Cronin A., Davis P., Felkewell T., Frazer A.,			
RA	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,			
RA	Hallroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,			
RA	James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,			

RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Stammers M., Squares R., Stevens S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grympey B.,
 RA Welter J., Vanstreels E., Rieger M., Schaefer M., Weller-Auer S.,
 RA Gabel C., Fuchs M., Fricz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leinhardt H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambolt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Laureau V., Motier S.,
 RA Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rocher M., Gallard C., Tallada V.A., Garçon A., Thode G.,
 RA Dada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Pothakkin J.,
 RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe.",
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL
 CC SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOSENSING SIGNAL
 CC TRANSMITTED THROUGH WISKI MAP KINASE.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL, L34881, AA67320.1, -.
 DR EMBL, AL031579, CA20880.1, -.
 DR HSSP, P35813, IA6Q.
 DR InterPro, IPR001932, PP2C-like.
 DR InterPro, IPR00222, PP2C.
 DR Pfam, PF00481, PP2C; 1.
 DR SMART, SM00331, PP2C_Sig, 1.
 DR SMART, SM00332, PP2C; 1.
 DR PROSITE, PS01032, PP2C; 1.
 KW Hydroxylase; Magnesium; Manganese; Multigene family.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 63 63 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 233 233 MANGANESE 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 370 AA; 40878 MW; DBDDB826F440AC50 CXC64;

Alignment Scores:
 Pred. No.: 1.4e-18 Length: 370
 Score: 362.00 Matches: 107
 Percent Similarity: 47.68% Conservatve: 47
 Best Local Similarity: 33.13% Mismatches: 110
 Query Match: 14.14% Indels: 59
 DB: 1 Gaps: 14

US-09-935-124a-1 (1-1422) x PP2C_SCHPO (1-370)

QY 407 GGATGATCTTGGCTGAAGGCTATGTGCTGAGCGGAGGTGAGAGGAGAGATGCA 466
 Db 18 GtAaPAPAGTTP-LeuHAPheGlyValSerHISmetGInGlyTPHAgILSerMetGcl 37
 QY 467 GGATGCCCAAGTCATCTGAGACATCAACCGAG-----GAGTGAAGCCCAATGTC 520
 Db 37 uAePAlaHISCyAlaLeuAlaSnPheHrAePserAenSerAenPProPioThr-- 56
 QY 521 CCTCATCTACGGGGTTTCATATTTTGGCTTTTGTATGAGACATGAGGAATTCGAGCCTC 580

Db 57 -----SerPheGlyValPheAePGLyHISGLyGLyAePAGValAl 71
 QY 581 AAAATTTCTGCACAGAAATTTGCATCAAACTTATCAGAAATTTCT-----AA 631
 Db 71 alyeTyrcysArgInHISleu---ProAePILeILeYserGInPProSerPheTrrly 90
 QY 632 AGGAGATGTAATCACTGTAGAGAAAACCTGAAGAGATGCTTTTGGACACTTTGAACA 691
 Db 90 gGLyAen-----TyRAePGLyAlaLeuYsSerGlyPheLeuAl 103
 QY 692 TACTGATGAAGTTCCTTAACAAGTTCACGACGAGAAAGCTGCGAAGAAGTGGCT 751
 Db 103 aAlaPhePnaAlaLeuWeGInAePArgAePmeGInIuAeP-----ProSerGlyCy 121
 QY 752 CACTGCCACGTGTGTTCTGCTGTAGAAC-----ATTCTTATATATGCCAATTCGAGAGA 808
 Db 121 eThrAlaHrThrAlaLeuILeValAlaPheISGLValleTyrcysAlaAenAlaGLyAs 141
 QY 809 TAGTGGGCAATCTTGTCTGTTATATGAGAGAGTCMAAACAATGACGCTTAAGCT 868
 Db 141 pSerArgThrValleuGLyArg-----LysGLyThrAlaGLuProLe 155
 QY 869 CAGCAAGAAGCATATCAACTCAGTATGAAGAGCGGATGAGATACAGAGGCTGAGG 928
 Db 155 userPheAePAlaSLyPProAenAenAePValGLyValAlaArgILeThrAlaAlaGLyG 175
 QY 929 AAACGTCAAGGATGGCGCTGTTTGGCGCTGACAGGTGCAGCTTCATTTGGGAGCG 988
 Db 175 yPheILaPhePheGlyArgValaenGlySerLeuAlaLeuSerArgAlaILeGLyAeP 195
 QY 989 GCAGTACAGCGCTCGGT-----GTCACCTGTGCGCGCA 1024
 Db 195 eGLuTyrcysAePserSerLeuProGLuYsGLInleValThrAlaPheProAs 215
 QY 1025 CATCAAGACGTGCCAGCGACCCCAATGACAGGATGATTTGTTGGCTGTGATGGCT 1084
 Db 215 pValAlaILeHISaenILeAePProAePAsPGLuPheLeuILeValaCyAePGLyIL 235
 QY 1085 CTTCAAGGCTTTTACCCCGCAAGAGCCGTGAATTCATTTGTCCTGTCGAGATGA 1144
 Db 235 eTrrAePcySLyPserSerGInGInValaGLuPheVal----- 248
 QY 1145 AAAGATCCAGACCGGGAAGGAAAGTCCGACCGGACCGCGCTTACGAGACCTGCA 1204
 Db 249 -----ArgArgGlyILeValAlaArgILeSer---LeuGLuValILeCyse 263
 QY 1205 CAGGTGGCCAACAAGCGGTCGACGGCGGCTG-----GCCGACAA 1246
 Db 263 uAenLeuWePArgPcySLyILeAlaSerAenSerGILuSerCyseGLyILeGLyCyAePAs 283
 QY 1247 GGTCACTGTGATGTGTGCGGATAGGACACTGAGAGGAGTGGCGCGGCGACGAGCACGC 1306
 Db 283 nMeThrILeCyAlleValAlaPheLeuHIS-----GLyArgGLyLeuGLuAeP-- 299
 QY 1307 ATGGTAT 1313
 Db 300 -TrrPtyr 301

RESULT 4
 FEM2_HUMAN STANDARD; PRT; 454 AA.
 ID FEM2_HUMAN
 AC P49593; Q96PM2;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
 DE (CamK2Pase) (hFEM-2).
 GN KIAA0015.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]

RA SEQUENCE FROM N.A.
 RX PubMed=11559703;
 RA Tan K.M.L., Chan S.L., Tan K.O., Yu V.C.;
 RT "The *Caenorhabditis elegans* sex-determining protein fem-2 and its
 RT human homologue hFEM-2 are C2/c14modulin-dependent protein kinase
 RT phosphatases that promote apoptosis.";
 RL J. Biol. Chem. 276:44193-44202(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=96051187; PubMed=7584026;
 RA Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
 RA Sato S., Nagase T., Seki N., Ishikawa K.-i., Tadota S.;
 RT "Prediction of the coding sequences of unidentified human genes. I.
 RT The coding sequences of 40 new genes (K1AA0001-K1AA0040) deduced by
 RT analysis of randomly sampled cDNA clones from human immature myeloid
 RT cell line KG-1.";
 RL DNA Res. 1:27-35(1994).
 RC -1- FUNCTION: Dephosphorylates and concomitantly deactivates CAM-
 CC kinase II activated upon autophosphorylation, and CAM-kinases IV
 CC and I activated upon phosphorylation by CAM-kinase kinase.
 CC Promotes apoptosis.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SUBUNIT: Associates with FLA14ha.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF305840; BAAL15579.1; -;
 DR EMBL; D13640; AAL02803.1; -;
 DR InterPro; IPR001932; PP2C-like.
 DR InterPro; IPR000222; PP2C.
 DR SMART; PF00481; PP2C; 1.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_S1G; 1.
 DR SMART; SM00333; PP2C_G; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydroxylase, Magnesium, Manganese, Apoptosis, Multigene family.
 FT METAL 101
 FT METAL 360
 FT METAL 404
 FT CONFLICT 202
 SQ SEQUENCE 454 Aa; 2456262333BC9CF CRC64;

 Alignment Scores:
 Pred. No.: 2,23e-18 Length: 454
 Score: 359.50 Matches: 126
 Percent Similarity: 42.63% Conservative: 65
 Best Local Similarity: 28.12% Mismatch: 146
 Query Match: 14.04% Indels: 111
 DB: 1 Gaps: 16

 US-09-935-124A-1 (1-1422) x FEM2_HUMAN (1-454)
 QY 129 CCGGAGCGCTCCGCCCGCGCGCGCGCGGGAAGAAGCTCAGAAAGACCCCTG----- 182
 Db 6 ProGlnLysSerSerPrometAlaSerGlyAlaGlnGlnThrProGlyPheLysAspThr 25
 QY 183 CTCCTTGATGACTCCCTCCGGCGGACGAGTACGTACGTACGATCAGGGGAGACCTTGCTT 242
 Db 26 LeuLeuGlnAspPheProAlaLeuLeuLeuAsnProGlu----- 37
 QY 243 TTTTGATGATCTCCACCGCGTACGAGTGGCGAT-----TCAGGT 281
 Db 38 ---AspProLeuPheProTpyLysAlaProGlyThrValLeuSerGlnGlnLysValGlnGly 56

[illegible]

DB 369 ValAlaGluGlu-----LeuValAlaAlaAlaArgGluValArgGlySerHis 403
 QY 1242 GACAACGTCATCTGATGTCGTCG 1265
 DB 404 AspaenilleThrValMetValVal 411
 RESULT 5
 P2C1 ARATH STANDARD; PRT; 434 AA.
 AC P49597; Q43717; Q94C87;
 DT 01-FEB-1996 (Rel. 33; Created)
 DT 15-JUN-2002 (Rel. 41; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Protein phosphatase 2C AB11 (EC 3.1.3.16) (PP2C) (Abscisic acid-insensitive 1).
 GN AB11 OR AT4G26080 OR F20B18.190.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI TaxId=3702;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT ASP-180.
 RC STRAIN=cv. Landsberg erecta.
 RX MEDLINE=94255767; PubMed=8197457;
 RA Meyer K., Leube M.P., Grill E.;
 RT "A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis thaliana."
 RL Science 264:1452-1455 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=leaf;
 RX MEDLINE=95007758; PubMed=7923358;
 RA Mindirios M., Katagiri F., Yu G.L., Ausubel F.M.;
 RT "The A. thaliana disease resistance gene Rps2 encodes a protein containing a nucleotide-binding site and leucine-rich repeats."
 RL Cell 78:1089-1099 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=leaf;
 RX MEDLINE=94255766; PubMed=7910981;
 RA Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F., Giraudet J.;
 RT "Arabidopsis ABA response gene AB11: features of a calcium-modulated protein phosphatase."
 RL Science 264:1448-1452 (1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Mayer K.F.X., Schellier C., Wambutt R., Murphy G., Volckaert G., Pohl T., Dueserhoef A., Striekema W., Entlian K.-D., Terryn N., Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M., Weisneltgatter M., de Simone V., Obermayer B., Macho R., Mueller M., Kreisel B., Deleney M., Pildomench P., Watson M., Schmidheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hohenseil J., Zimmermann W., Medler H., Ridley P., Langham S.-A., McCullagh B., Bligham L., Robben J., Van der Schueren J., Grymoprez B., Chuang Y.-D., Vandenbusche F., Braeken M., Weltjens I., Voet M., Baetiaens I., Aert R., Defoor E., Weltzenegger T., Bothe G., Rampegerger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., van Staveren M., Dirks W., Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koeltter P., Bernieris S., Hempel S., Feldausch M., Lamberch S., Van den Daele H., De Keyser A., Buysheert C., Gielen J., Villarroel R., De Clercq R., Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Alien S., Clark L., Doggett J., Hall S., Kay M., Lennard N., Mcay K., Mayes R., Petrelet A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Borkova D., Bioecker H., Scharfe M., Grimm M., Loehner T.-H., Doebe S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fartmann B., Grandenath K., Danner E., Herzl A., Neumann S., Argitlou A., Vitale D., Liguori R., Piravandi E.,

RA Massenet O., Quigley F., Clabaud G., Mendlein A., Felder R., Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., RA Gidbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A., RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielle C., RA Frisman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., RA Parnell L., Dedha N., Gnoj L., Schütz K., Huang E., Spiegel L., RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J., RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., RA Lacroelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., RA Mixx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L., RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C., RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C., RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., RA Granat S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A., RA Chen E., Marra M., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana";
 RL Nature 402:769-777 (1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the RSP consortium (Salk/Stanford/PGSC)."
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN ABSICISIC ACID (ABA) SIGNALING PATHWAY.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC CC
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 CC -----
 CC EMBL; X78886; CAAS5484.1; -;
 CC EMBL; U12856; AAA50237.1; -;
 CC EMBL; X77116; CA534383.1; -;
 CC EMBL; AL049483; CAB39673.1; -;
 CC EMBL; AL161564; CAB79463.1; -;
 CC EMBL; AY035073; AAK59578.1; -;
 CC HSSP; P35813; 1A60.
 CC InterPro; IPR002048; EF-hand.
 CC InterPro; IPR001932; PP2C-like.
 CC InterPro; IPR002221; PP2C.
 CC Pfam; PF00481; PP2C; 1.
 CC SMART; SM00331; PP2C_SIG; 1.
 CC SMART; SM00332; PP2C; 1.
 CC PROSITE; PS00016; EF_HAND; 1.
 CC PROSITE; PS01032; PP2C; 1.
 CC KX HydroLase; Magnesium; Manganese; Multigene family; Calcium-binding.
 CC FT CA BIND 93 104
 CC FT DOMAIN 417 420
 CC FT VARIANT 180 180
 CC FT
 CC CONFLICT 24 24
 CC CONFLICT 105 105
 CC SEQ SEQUENCE 434 AA; 47505 MM; 4A4CS4F04195F572 CRC64;
 Alignment Scores:
 Pred. No.: 7.05e-18 Length: 434
 Score: 352.50 Matches: 125
 Percent Similarity: 44.71% Conservative: 65

Best Local Similarity: 29.41%
 Query Match: 13.77%
 DB: 1
 Mismatches: 148
 Indels: 87
 Gaps: 19
 US-09-935-124a-1 (1-1422) x P2C1 ARATH (1-434)

QY 105 GACCTTTCGGGAGCTTCGAGCCGAGCCGCG--TCGCGCGCGCGCGCGGAGAA 161
 DB 45 AspleumetvalserleuprogluintheserCysSerValserglSerHieglYser 64
 QY 162 GAAGCTCAGAAAGAGACCCCTGCTTGTATGATCCTCCGCGGAGCAAGTACTGA 221
 DB 65 GluserArglyValleulleSerArglleAenserProAemleuMetleuSer 84
 QY 222 GCATCAGGGGACCTTGTCTTGTATGATCTCCACCGCTAGACAGTGGCGAT----- 275
 DB 85 AlaAlaAlaAspIleValValValp-----IleSerAlaGlyAspGluIle 100
 QY 276 TCAGGTTCTTCGACATCAATTCACAGATGTA--AAGACTGAAGGAGAAAGAGCA 332
 DB 101 AenglySerAspIleTherSerGluYelMetleuSerArgHie----- 116
 QY 333 AAGAGAAAACCTCCGAGAGAGAGAAATGACATGCAAGCTTGCGAAAAGAAATT 392
 DB 117 -----SerArgSerleuPheGluPheLys--- 124
 QY 393 TGTAAAGCTTCCTCGATGATTTGTGTGAGAGGCTATGTGCTGAGCGGAGGTGAG 452
 DB 125 -----SerValProleuYrglyPheTherSerleCys-----GlyArg 137
 QY 453 AGGAGAGATGACAGATGCCACGCTATCTGAAAGCATGACCGGAGAGTGAAGCCC 512
 DB 138 ArgProGluMetGluAspAla-----ValSerHieProArgPheleuGluSer 154
 QY 513 CCATCGTCCCTCAT-----ACTCGGCTTCATATATTTGCT 548
 DB 155 SerSerGlySerMetleuAspGlyArgPheAspProGluSerAlaAlaHiePheGly 174
 QY 549 GTTGTGATGACATGACAGATTCGAGCTCAAAATTTGTGACAGAAATTTGACATCA 608
 DB 175 ValYAspGlyHieGlySerGluValAlaAemTyrCysArgGluArgMetHieLeu 194
 QY 609 AACTTATCAGAAATTTCCATA-----GGAGATGTAAATCAGT 647
 DB 195 AlaLeuAlaGluGluIleAlaLeuGlyLeuPheMetleuCysAspGlyAspThr---Trp 213
 QY 648 GTAGAGAAACCGTGAAGAGATGCTTTGAGACATTCAGACATCTGATGAAGATTG 707
 DB 214 LeuGluYstrP--LysYAlaLeuPheAsnSerPheLeuArgValAspSerGluIle 232
 QY 708 CTTAAACAGCTTCAGCCAGAGACCTGCTGAAAAGTGGTCCATGCCACGTGTGT 767
 DB 233 GluserValAlaProGluThrVal-----GlySerTherSerValAla 247
 QY 768 CTGGCTGAGACATCTTATATATGCGAACCTCGAGATAGTCGGGCAATCTGTGT 827
 DB 248 ValValPheProSerHieIlePheValAlaAsnCyGlyAspSerArgAlaValLeuCyG 267
 QY 828 CGTTATATGAGAGAGATCAAAAACATGACCTTAAGCTTCAGGAAAGAGCATATTC 887
 DB 268 Arg-----GlyYserThraLeuProLeuSerValAspHieLysPro 281
 QY 888 ACTCAGTATGAGAGCGGATGAGATGACAGAGCTGAGAGAAAGCTC-----AGG 938
 DB 282 AsparGlyAspGluAlaAlaArglleGluAlaAlaGlyLeuValIleGlnTrpAan 301
 QY 939 GATGGCGCTGTTGGGCGTGTGAGGTGTCACGCTCATTTGGGAGCGGCGAGTCAAG 998
 DB 302 GlyAlaArgValPheGlyValleuAlaMetSerArgSerlleGlyAsp--ArgYrLeu 320
 QY 999 CGCTGGGTGACCTCTGTGCGGACATGACAGCGTGCAGTCAACCCCATGACAG 1058
 DB 321 LysProSerIleIleProAspProGluValThrAlaValIleArgValIleGluAsp 340

QY 1059 TTCAATTTGTCCTGTGATGCGCTCTTCAAGCTTTTACCCGAGAAAGCCGTGAC 1118
 DB 341 CysLeuIleLeuAlaSerAspIleValTrpAspValMetThrAspIleGluAlaCysGlu 360
 QY 1119 TTCATC-----TTGTCC 1130
 DB 361 MetAlaArglyAspIleLeuLeuThrIleLysLysAsnAlaValAlaGlyAspAlaSer 380
 QY 1131 TGCTCGAGATGAAAGATCCAGACCCGAGAGAGGAAGTCCGACGCCGCGCTAC 1190
 DB 381 LeuLeuAlaAspIleLys-----ArglySerGluLys-----AspProAlaAla 395
 QY 1191 GAACAGCCTGCAACAGCGTGGCCCAACAGCGGTGACGAGCGGCGCTCGGCGCAACGTC 1250
 DB 396 MetSerAlaAlaGluTrpLeuSerLysLeuAlaIleGlnArgIleSerLysAspAsnIle 415
 QY 1251 ACTGTAGTGGGTG 1265
 DB 416 SerValValValVal 420

RESULT 6
 P2C2 CABEL STANDARD; PRT; 356 AA.
 AC P49596;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C).
 GN T23F11.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Swaburne J.;
 RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP REVISIONS.
 RA Durbin R.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; Z46343; CAA86456.2; -.
 DR HSSP; P35813; IAG6.
 DR WormPep; T23F11.1; CE24009.
 DR InterPro; IPR001932; PP2C-like.
 DR InterPro; IPR002222; PP2C.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C; sig. 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein; Hydrolase; Magnesium; Manganese.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 59 59 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 228 228 MANGANESE 2 (BY SIMILARITY).
 FT METAL 277 277 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 356 AA; 39064 MW; EDCB0841CFB026B5 CRC64.

Alignment Scores:

Pred. No.: 1,54e-17 Length: 356
 Score: 347.50 Matches: 103
 Percent Similarity: 48.63% Conservative: 57
 Best Local Similarity: 31.31% Mismatches: 108
 Query Match: 13.57% Indels: 61
 DB: 1 Gaps: 13

US-09-935-124A-1 (1-1422) x P2C2_CABEL (1-356)

```

QY 372 GAGCTTGAGAAAAGAAAGTCTTAAGCCTCTTGCGTATCTTGGTCTGAAGGCTAT 431
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 3 GlnThrLeuSerGluProValThrLysLysGluSerValSerCysAlaasnGluLeuTyr 22
QY 432 GTGGCTGAG-----CGGAAGGCTGAGAGGAGAGATGAGAGATGCCCGCATC 482
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 23 LeuValGlySerSerCysMetGlnGlyTPRgValAspMetGluAspAlaHisThrHis 42
QY 483 CTGAACGACATCACCGAGAGGTGTAGCCCCCATGCTCCCTCATTACTCGGGTTTCAT 542
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 43 LeuLeuSerLeuProAspAsp-----ProLysCysAlaPhe 54
QY 543 TTTGCTTTTGGATGAGAGGATGAGGATTCGAAATTCCTGACAGATTTG 602
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 55 PheAlaValTyrAspGlyHisGlyGlySerValSerGlnTyrSerGlyLeuAsnLeu 74
QY 603 CATCAAAACTTATC-----AGAAATTTCCTAAGAGAGATGA---ATCAGTGTAGAG 653
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 75 HisLysLysValValAlaGlnLysGluPheSerGlnGlyAsnMetLysGluAlaLeu 94
QY 654 AAAACCGTGAAGAGATGCTTTTGAACACTTTCAGCATACTGATGAGAGATTCCTTAA 713
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 95 LysGlyPheLeuGlu-----LeuAspGlnGlnMetArgValAspGluThrLysAsp 112
QY 714 CAAGCTTCAGCCAGAGAGCTGCTGAAAAGATGGCTCCACTGCCACGCTGTTCTGCT 773
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 113 AspValSer-----GlyThrThrAlaValAlaValLeuLeu 124
QY 774 GTAGACAACTTTATATTGCGCAACTCGAGATAGTCGGGCAATCTTGTCGTTAT 833
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 125 LysGlnGlyAspValTyrCysGlyAsnAlaGlyAspSerThrAlaValSerValVal 144
QY 834 AATGAGAGAGTCAAAAACATGACAGCTTAAGCTTCAGCAAAAGCATTAATCACTCAG 893
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 145 GlyGlu-----AlaArgProLeuSerPheAspHisLysProSerHis 158
QY 894 TATGAAGAGCGATGAGATACAGAGAGCTGGAGAGAAAGTACAGGATGGCTTTTG 953
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 159 GluThrGluAlaArgArgGlyLeuAlaAlaGlyGlyTyrValGluPheAsnArgValAsn 178
QY 954 GAGCTGCTAGAGGTGTCAGCTCATTTGGGAGCGGCGCATCAAGCGCTGCGGT----- 1007
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 179 GlyAsnLeuAlaLeuSerThrAlaLeuGlyAspPheAlaPheLysAsnGlyAspThrLys 198
QY 1008 -----GTCACTCTGTGCGCGCATCAGACGCTGACAGTGAAGCCCC 1049
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 199 ProAlaGluGluGlnLeuValThrAlaPheProAspValIleThrAspLysLeuThrPro 218
QY 1050 AATGACAGGTCATTGTTGCTGCTGATGGCTTTCAAGGCTTTTACCCAGAGAA 1109
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 219 AspHisGluPheIleValLeuAlaCysAspGlyIleTyrAspValMetThrAsnGlnGlu 238
QY 1110 GCCGTGAACCTCATCTTGCTGCTGTCGAGATGAAAGATCCAGACCGGGAGAGGAAG 1169
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 239 ValValAspPheVal-----ArgLys--Lys 246
QY 1170 TCCGAGCGGAGCGCCGCTACGAGAGCGCTGCAACAGGCTGGCCAAAGCGCGTG-- 1226
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 247 LeuAlaGluLysLysAspProGlnSerIleCysGluGluLeuLeuThrArgCysLeuAla 266
QY 1227 -----CAGCGGGGC-----TCGCGCCAGCAACGTCATCTGTGATGGTGGCGATA 1271
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 267 ProAspCysGlnMetGlyGlyLeuGlyCysAspAsnMetThrValValLeuVal----- 284
  
```

QY 1272 GGGCACTGAGGGTGGCGCGCGCCAG 1298
 DB 285 -----GlyLeuLeuHisGlyGln 290

RESULT 7

P2CA_BOVIN

ID P2CA_BOVIN STANDARD; PRT; 382 AA.

AC 062829;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (P2C2-alpha).

GN PPM1A.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Retina;

RX MEDLINE=98146173, PubMed=9486768;

RA Klump, S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;

RT "Protein phosphatase type-2C isozymes present in vertebrate retinac:

RT purification, characterization, and localization in photoreceptors.";

RL J. Neurosci. Res. 51:328-338(1998).

CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.

CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +

CC phosphate.

CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.

CC -1- SUBUNIT: MONOMER (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE P2C FAMILY.

CC -----

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CC -----

DR HSBP; A005457; CAA0554.1; -.

DR HSBP; P35813; IAG0.

DR InterPro; IPR001932; P2C-like.

DR InterPro; IPR000222; P2C.

DR Pfam; PF00481; P2C; 1.

DR SMART; SM00331; P2C_SIG; 1.

DR SMART; SM00332; P2C; 1.

DR PROSITE; PS01032; P2C; 1.

KW Hydrolyase; Magnesium; Manganese; Multigene family.

FT METAL 37 38 MANGANESE 1 (BY SIMILARITY).

FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).

FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).

FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).

FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).

SQ SEQUENCE 382 AA; 42529 MW; A716B3FA0B7821C2 CRC64;

Alignment Scores:

Pred. No.: 3.9e-17 Length: 382
 Score: 342.00 Matches: 101
 Percent Similarity: 49.33% Conservative: 47
 Best Local Similarity: 33.67% Mismatches: 104
 Query Match: 13.36% Indels: 48
 DB: 1 Gaps: 12

US-09-935-124A-1 (1-1422) x P2CA_BOVIN (1-382)

```

QY 417 GGTGGAAGGGGTATGTCGTCGAGCGGAAGGTCGAGAGAGATGACAGATGCCAC 476
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 21 GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTPRgValGluMetGluAspAlaHis 40
QY 477 GTCATCTGAACGACATCACCGAGAGGTGTAGCCCCCATGCTCCCTCATTACTCGGGTT 536
  
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Db 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGluThr---TTP 53
QY 537 TCATATTTTGTCTTTTGTATGATGACATGAGAAATTCAGACCTCAAAATTTGTCTGCACAG 596
Db 54 SerPhePheAlaValIleArgGlyHisAlaGlySerGlnValAlaIleValTyrCysGlyGlu 73
QY 597 AATTTCATCAAACTTATTCAGAAATTTCCCT---AAAGAGAT-----GTATTCAGT 647
Db 74 HisLeuLeuAspHisIleIleThrAsnAsnGlnAspPheGlySerAlaGlyAlaProSer 93
QY 648 GTAGAGAAAACCTGAGAGATGCGCTTTTGTGACATTTCAAGCATATGATGAAGATTTC 707
Db 94 ValGlu---AsnValIleAsnGlyIleArgThrGlyPheLeuGluIleAspGlnHisMet 112
QY 708 CTTAAACAGACTTCCAGACCAAGCCTGGAAGAGGCTGACATGCGACGCTGCTT 767
Db 113 ArgValMetSerGluValLeuHisGlyAlaAspArgSerGlySerThrAlaValAlaGlyVal 132
QY 768 CTGGCTGTAGACAAATCTTATATGATCCCACTCGGAGATAGCGGGCAATCTTGCT 827
Db 133 LeuIleSerProGlnHisIleThrPheIleAsnGlySerGlyAspSerAlaGlyLeuLeuCys 152
QY 828 CATTATATGAGAGATGCAAAAACATGACGCTTAAGCTTCAAGAAAGCATTAATCCA 887
Db 153 Arg-----AsnArgIleValIleTyrPhePheThrGlnAspHisIleValPro 166
QY 888 ACTCACTATGAAGACCGGATGATGATACAGAAAGCTGAGAAACGTCAAGGATGAGCCT 947
Db 167 SerAsnProLeuGlnIleValArgIleGlnAsnAlaGlyGlySerValMetIleGlnArg 186
QY 948 GTTTTGGGCTGCTAGAGAGTGTCAAGCTCCATTTGGGAGCGGACAGTACAAAGCTGCTG 1004
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheArgTyrIle---CysVal 205
QY 1005 -----GGTGTACC-----TCTGTCCCGGACAGTACGA 1031
Db 206 HisGlyIleGlyProThrGlnGlnLeuValSerProGluProGluValHisAspIleGln 225
QY 1032 CGGTCCAGCTGATCCCAATGACAGGTGATTTTGTGCGCTGATGGGCTTTCAG 1091
Db 226 ArgSerGlu-----GluAspArgGlnPheIleIleLeuAlaCysAspArgIleTyrParg 243
QY 1092 GTCTTTAACCACAGAAAGACCGTGAATCTTCTGCTGCTGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGlnGluLeuCysAspPheValArgSerArgLeuGluValIleThrAspArg 263
QY 1146 AAGATCCAGACCCGGGAAAGGAAAGTCCGACGCCGCTTACGAAGACCTGCAAC 1205
Db 264 -----LeuGluIleValIleCysAsn 269
QY 1206 AGGCTGAGCCACAGACGCGGTGACGCGGCTCGGACGACAGTCACTGATGCTGCTG 1265
Db 270 GluValValAspThrCysLeuTyrIleGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 8
FEM2_RAT STANDARD; PRT; 450 AA.
AC Q9WVR7;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
DE (Cam-kinase phosphatase) (CamKpase).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
MEDLINE=99279559; PubMed=10348902;
KItani T., Ishida A., Okuno S., Takeuchi M., Kameehita I.,

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RA Fujisawa H.;
RT "Molecular cloning of Ca2+/calmodulin-dependent protein kinase
RT phosphatase.";
RL J. Biochem. 125:1022-1028(1999).
CC -1- FUNCTION: Dephosphorylates and concomitantly deactivates Cam-
CC kinase II activated upon autophosphorylation, and Cam-kinase IV
CC and I activated upon phosphorylation by Cam-kinase kinase.
CC Promotes apoptosis.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: Associates with P1alpha (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AB023634; BA82477.1; -.
CC InterPro: IPR000222; PP2C.
CC InterPro: IPR001932; PP2C-like.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00332; PP2C; 1.
CC SMART; SM00331; PP2C-SIG; 1.
CC PROSITE; PS01032; PP2C; 1.
CC KW Hydroxylase; Magnesium; Manganese; Apoptosis; Multigene family.
CC DOMAIN 99 109 POLY-GLU.
CC FT METAL 356 356 MANGANESE 2 (BY SIMILARITY).
CC FT METAL 400 400 MANGANESE 2 (BY SIMILARITY).
CC FT METAL 450 450 MANGANESE 2 (BY SIMILARITY).
CC SQ SEQUENCE 450 AA; 49165 MW; 67626542F32B2FD0 CRC64;

Alignment Scores:
Pred. No.: 4,41e-17 Length: 450
Score: 341.50 Matches: 124
Percent Similarity: 44.31% Conserves: 63
Best Local Similarity: 29.38% Mismatches: 160
Query Match: 13.34% Indels: 75
DB: 1 Gaps: 16

US-09-935-124A-1 (1-1422) x FEM2_RAT (1-450)
QY 108 CTTCTTGGGAGACCTCGCGGAGCCGAGCGCTCGCGGCTCGCGGAGAAAGACT 167
Db 25 LeuLeuGlnAspPheProAlaProLeuSerLeuGlnSerProLeuProTyrIle----- 42
QY 168 CAGAAAGACCCCTGCTCTTTGATGATCTCCCTCGGACGACGATGACTGATCA 227
Db 43 ValProGlyThrValIleGlnIleGlnIleValIleGlnIleLeuThrIleValMet 62
QY 228 GGGGACCTTTGCTTTTGTATGATCTCCACCCGCTGACGATGCGATTCAGGTTCTCTT 287
Db 63 GlyPhe---LeuGlySerArgAsnAlaProProAlaValAlaIle-----AlaIleValThr 79
QY 288 GCCCATCATATATCCAGATGTTAAAGACTGAAGGAGAAAGAGCAAAAGAAACCTCC 347
Db 80 HisGluAlaIleSerGlnIleLeuGlnIleThrAspSerGlnIlePheValIleProGlu 99
QY 348 GAGGAGAGAGAGAGATGCGAGTGAAGAG-----CTTGTGAAAAGAAA 389
Db 100 GlnGlnGlnGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 119
QY 390 -----GTTGTAAACCTCTTCGCTGATC 413
Db 120 GlyLeuSerArgSerPhePheAsnGlySerProGluValIleCysSerGlnIleGlnIleArg 139
QY 414 TTTGCTCTGAAGGCTATATGCTGACGGAG----- 446
Db 140 ValProLeuThrAlaGlnAlaProGlnArgIleValIleValSerIleHisAlaIleArg 159

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Db 113 ArgValMetSerGluValGlyHisGlyAlaAspArgSerGlySerThrAlaValAlaGlyVal 132
Qy 768 CTGGCTGTAGACAACTTTCTTATTATTCGACATCTCGGAGATAGTCCGGCAATCTTGCT 827
Db 133 LeuIleSerProGlnHisThrTyPheIleAsnCyGlyAspSerArgGlyLeuLeuCyS 152
Qy 828 CGTTATATATGAGAGATCAAAAACATGACGCTTAAAGCTTACGCAAAAGACATATCCA 887
Db 153 Arg-----AsnArgLysValHisPhePheThrGlnAspHisGlyPro 166
Qy 888 ACTCACTATGAAAGCGGATGAGATACAGAAAGCTGAGAAAGCTGACGAGATGGCGCT 947
Db 167 SerAsnProLeuGlnLysGlnArgIleGlnAsnAlaGlySerValMetIleGlnArg 186
Qy 948 GTTTGGGCGCTGAGGTGTCAGGCTCCATTCGAGGAGCGGACATACACCGCTGC--- 1004
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTyrLys---CysVal 205
Qy 1005 -----GGTGTACC-----TCGTGCCCGGACATCAGA 1031
Db 206 HisGlyLysGlyProThrGlnGlnLeuValSerProGlnProGlnValHisAspIleGlu 225
Qy 1032 CGCTGCACCTGACATCCCAAGACAGATGTTTGTGGCTGTGATGGGCTCTTCAG 1091
Db 226 ArgSerGlu-----GluAspAspGlnPheIleLeuAlaCyAspGlyIleTyrAsp 243
Qy 1092 GTCTTATCCCAAGANAGCCGTGACTTCTTCTCTCTGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGlnGlnLeuCyAspPheValArgSerArgLeuGlnValThrAspAsp 263
Qy 1146 AAGATCCAGACCCGGGAAAGGAGAGTCCGACGCCGCTTACGAAAGACGCTTCAG 1205
Db 264 -----LeuGlnLysValCyAsn 269
Qy 1206 AGCTGCGCAACAGACGCGGTGACGCGGCTCGGCGCAACGTCATGTAGTGTG 1265
Db 270 GluValValAspThrCysLeuTyrGlyGlySerArgAspAspMetSerValIleLeuIle 289
RESULT 10
P2CA RAT STANDARD; PRT; 382 AA.
AC P20650;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein phosphatase 2C, alpha isoform (BC 3.1.3.16) (P2C-alpha) (IA)
GN (Protein phosphatase 1A).
GN PPM1A OR PPM1A OR P2C1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=89184515; PubMed=2538815;
RA Tamura S., Lynch K.R., Larner J., Fox J., Yasui A., Kikuchi K.,
SA Suzuki Y., Tsuniki S.;
RT "Molecular cloning of rat type 2C (1A) protein phosphatase mRNA."
RT Proc. Natl. Acad. Sci. U.S.A. 86:1796-1800(1989).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE P2C FAMILY.
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CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL: J04503; AAA1917.1; -.
CC PIR: A32399; A32399.
DR HSSP; P35815; 1A60.
DR InterPro; IPR001932; P2C-like.
DR InterPro; IPR000222; P2C.
DR Pfam; PF00481; P2C; 1.
DR SMART; SM00331; P2C_SIG; 1.
DR PROSITE; PS01032; P2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family.
FT METAL 37
FT METAL 38
FT METAL 60
FT METAL 239
FT METAL 282
SQ SEQUENCE 382 AA; 42416 MW; C1386B935374F89 CRC64;
Alignment Scores:
Pred. No.: 5,446-17 Length: 382
Score: 340.00 Matches: 101
Percent Similarity: 49.33% Conservative: 47
Best Local Similarity: 33.67% Mismatches: 104
Query Match: 13.28% Indels: 46
Gaps: 12
US-09-935-124A-1 (1-1422) x P2CA_RAT (1-382)
Qy 417 GGTCTGAAGGGCTATGTGTGCTAGCGGAAGGTGAGAGGAGATGACAGATGCCAC 476
Db 21 GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTyrArgValGlnLeuGlnAspAlaHis 40
Qy 477 GTCATCTCTGAACGACATCAACCGAGAGGTGTAGGCCCCCATCGTCCCTCATTAATCGGGTT 536
Db 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGlnThr---Tyr 53
Qy 537 TCATATTTTCTGTTTGTATGATGACATGAGAAATTCGACCTCAAAATTTCTGACAG 596
Db 54 SerPhePheAlaValTyrAspGlyHisAlaGlySerGlnValAlaTyrCysCysGlu 73
Qy 597 AATTGGATCAAACTTATTCAGAAATTTCT---AAAGAGAT-----GTATTCAGT 647
Db 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheLysGlySerAlaGlyAlaProSer 93
Qy 648 GTAAGGAAAACCGTGAAGAGATGCTTTTGGACCTTTCAAGATCTATGAGAAGTTC 707
Db 94 ValGlu---AsnValLysAsnGlyLysThrGlyPheLeuGlnLysAspGlnHisMet 112
Qy 708 CTTAAACAGCTTCACCGCAAGAGCTTCGGAAGATGGCTTCACCTCCACGTTGTT 767
Db 113 ArgValMetSerGluLysHisGlyAlaAspArgSerGlySerThrAlaValAlaGlyVal 132
Qy 768 CTGGCTGTAGACAACTTTCTTATTATTCGACATCTCGGAGATAGTCCGGCAATCTTGCT 827
Db 133 LeuIleSerProGlnHisThrTyPheIleAsnCyGlyAspSerArgGlyLeuLeuCyS 152
Qy 828 CGTTATATGAGAGATCAAAAACATGACGCTTAAAGCTTACGCAAAAGACATATCCA 887
Db 153 Arg-----AsnArgLysValHisPhePheThrGlnAspHisGlyPro 166
Qy 888 ACTCACTATGAAAGCGGATGAGATACAGAAAGCTGAGAAAGCTGACGAGATGGCGCT 947
Db 167 SerAsnProLeuGlnLysGlnArgIleGlnAsnAlaGlySerValMetIleGlnArg 186
Qy 948 GTTTGGGCGCTGAGGTGTCAGGCTCCATTCGAGGAGCGGACATACACCGCTGC--- 1004
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTyrLys---CysVal 205
Qy 1005 -----GGTGTACC-----TCGTGCCCGGACATCAGA 1031
Db 206 HisGlyLysGlyProThrGlnGlnLeuValSerProGlnProGlnValHisAspIleGlu 225


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OY 1032 CGCTGCCAGCTGACCCCAATGACAGCTTCATTGTTGGCTGTGATGGCTCTTCAAG 1091
    |||
    |||
    |||
Db 226 ArgSerGlu-----GluAspAspGlnPheIleIleLeuAlaCysAspGlyIleTyrAsp 243
OY 1092 GTCTTACCCCAAGAACCCGCGAATCTTCATCTTCTGCTGTGAG-----GATGAA 1145
    |||
    |||
    |||
Db 244 ValMetGlyAsnGlnGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 263
OY 1146 AAGATCCAGACCCCGGAGGAGAGTCCGACGCCGCGCTACGAGACAGCTTGCAAC 1205
    |||
    |||
    |||
Db 264 -----LeuGlnIuysValCysAsn 269

RESULT 11
P2CA_MOUSE STANDARD; PRT; 382 AA.
ID P2CA_MOUSE
AC P49443;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-1999 (Rel. 39, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (P2C-alpha) (1A)
DE (Protein phosphatase 1A).
GN PPM1A OR PPM1A.
OS Mus musculus (Mouse).
OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId10090;
RN (1)
RN SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=94333828; PubMed=8056349;
RA Kato S., Kobayashi T., Terasawa T., Ohnishi M., Sasahara Y.,
RA Kanamaru R., Tamura S.;
RT "The cDNA sequence encoding mouse Mg2+ -dependent protein phosphatase
RT alpha.";
RL Gene 145:311-312(1994).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE P2C FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL; D28117; BA005662.1; -.
DR HSSP; P35813; 1A6O.
DR MGD; MGI:99878; Ppm1a.
DR InterPro; IPR001932; P2C-like.
DR InterPro; IPR000222; P2C.
DR Pfam; PF00481; P2C; 1.
DR SMART; SM00331; P2C_SIG; 1.
DR SMART; SM00332; P2C; 1.
DR PROSITE; PS01032; P2C; 1.
KW Hydrolyase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 382 AA; 42432 MW; DC206610E1583870 CR64;

Alignment Scores: 7.58e-17 Length: 382
Pred. No.:

```

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Score: 338.00 Matches: 99
Percent Similarity: 48.67% Conservative: 47
Best Local Similarity: 33.00% Mismatches: 106
Query Match: 13.20% Indels: 48
DB: 1 Gaps: 11

US-09-935-124A-1 (1-1422) x P2CA_MOUSE (1-382)
OY 417 GGTCTGAAGGGCTATGATGCTGAGCGGAGGTGAGAGGAGAGATGACAGATCCGAC 476
    |||
    |||
    |||
Db 21 GlyLeuAaGlyrGlyLeuSerSerMetGlnGlyTyrAspValGluMetGluAspIleHis 40
OY 477 GTCATCTGAAACGACATGACCGAGAGTGTAGGCCCCCATGCTCCCTCATTAATCGGGT 536
    |||
    |||
    |||
Db 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGlnIuThr---Tyr 53
OY 537 TCATATTTTTCGCTTTTGTATGATGAGATGAGATTCAGCTCAATTAATTGCTGCACAG 596
    |||
    |||
    |||
Db 54 SerPhePheAlaValTyrAspGlyHisAlaGlySerGlnValAlaLeuTyrCysGly 73
OY 597 AATTGTCATCAAACTTATATCAGAAATTTCTCT-----AAAGAGATGTAATTCAGT 647
    |||
    |||
    |||
Db 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheAspGlySerAlaGlyAlaProSer 93
OY 648 GTAGAGAAAACCGTAGAGAGATGCTTTTGACACTTTCAAGCATATGATGAGAGATTG 707
    |||
    |||
    |||
Db 94 ValGlu---AsnValIuysAsnGlyIleArgThrGlyPheLeuGlnIleAspGlnHisMet 112
OY 708 CTTAAACAAGCTTCCAGCCAGAAAGCTGCGGAAGATGGGTCCACTGCGCACGTTGT 767
    |||
    |||
    |||
Db 113 ArgValMetSerGlnIuysAspHisGlyIleAspAspSerGlySerThrAlaValGlyVal 132
OY 768 CTGGCTGTAGACAAATCTTATATTCGCAACTCGGAGATAGTCGGGCAATCTTGTGT 827
    |||
    |||
    |||
Db 133 LeuIleSerProGlnHisIleThrTyrPheIleAsnGlyAspSerArgGlyLeuLeuCys 152
OY 828 CGTTATTAATGAGAGAGTCAAAACATGCAGCTTAAGCTTCAGCAAAAGCATATTCGA 887
    |||
    |||
    |||
Db 153 Arg-----AsnArgIuysValHisPhePheThrGlnAspIleIuysPro 166
OY 888 ACTCAGTATGAAGAGCGGATGAGTATACAGAAAGCTGAGAGAAAGTCAAGGATGGGCT 947
    |||
    |||
    |||
Db 167 SerAsnProLeuGlnIuysGlnArgIleGlnAsnAlaGlyIleSerValMetIleGlnArg 186
OY 948 GTTTGGGCGTGTGAGAGTGTGACGCTCATTTGGGGAGCGGAGTACAGAGCGCTG--- 1004
    |||
    |||
    |||
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTyrIuys---CysVal 205
OY 1005 -----GGTGTACC-----TTGTGCCCGACATTCAGA 1031
    |||
    |||
    |||
Db 206 HisGlyIuysGlyProThrGlnIuysValSerProGlnProGlnValHisIleAspIleGln 225
OY 1032 CGCTGCCAGCTGACCCCAATGACAGCTTCATTGTTGGCTGTGATGGCTCTTCAAG 1091
    |||
    |||
    |||
Db 226 ArgSerGlu-----GluAspAspGlnPheIleIleLeuAlaCysAspGlyIleTyrAsp 243
OY 1092 GTCTTACCCCAAGAACCCGCGAATCTTCATCTTCTGCTGTGAG-----GATGAA 1145
    |||
    |||
    |||
Db 244 ValMetGlyAsnGlnGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 263
OY 1146 AAGATCCAGACCCCGGAGGAGAGTCCGACGCCGCGCTACGAGACAGCTTGCAAC 1205
    |||
    |||
    |||
Db 264 -----LeuGlnIuysValCysAsn 269

RESULT 12
P2CA_HUMAN STANDARD; PRT; 382 AA.
ID P2CA_HUMAN
AC P35813; 075551;
DT 01-JUN-1994 (Rel. 29, Created)

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DT 01-JUN-1994 (Rel. 29, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE (Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IN
OS PPM1A OR PPM1A.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RX MEDLINE=92182001; PubMed=1311954;
RA Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;
RT "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and
RL comparative analysis of amino acid sequences";
RN Biochim. Biophys. Acta 1130:100-104 (1992).
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-2).
RX MEDLINE=98372386; PubMed=9707433;
RA Takekawa M., Maeda T., Saito H.;
RT "Protein phosphatase 2Calpha inhibits the human stress-responsive p38
RL and JNK MAPK pathways";
RN EMBO J. 17:4744-4752 (1998).
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RX TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=97157470; PubMed=9003755;
RA Das A.K., Helps N.R., Cohen P.T.W., Barford D.;
RT "Crystal structure of the protein serine/threonine phosphatase 2C at
RL 2.0-A resolution";
EMBO J. 15:6798-6809 (1996).
CC -1- FUNCTION: Enzyme with a broad specificity.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: Binds 2 magnesium or manganese ions.
CC -1- SUBUNIT: MONOMER.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-1 (SHOWN HERE) AND ALPHA-
CC 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL; S87759; AAB21784.1; -;
DR EMBL; AF070670; AAC28354.1; -;
DR EMBL; BC026691; AAH26691.1; -;
DR PIR; S22423; S22423.
DR Genem; HGNC:9275; PPM1A.
DR MIM; 606108; -;
DR PDB; 1A6Q; 27-MAY-98.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_Sig; 1.
DR SMART; SM00332; PP2CG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family;
KW Alternative splicing; 3D-structure.
FT METAL 37
FT METAL 38
FT METAL 60
FT METAL 239
FT METAL 282
FT METAL 324
FT VARSPLIC 318 324
FT EITKOG -> GGSFNKK (IN ISOFORM ALPHA-2).

FT VARSPLIC 325 382 MISSING (IN ISOFORM ALPHA-2).
SQ SEQUENCE 382 AA; 42447 MW; D48EF508BA476687 CRC64;
Alignment Scores:
Pred. No.: 1,06e-16 Length: 382
Score: 336.00 Matches: 100
Percent Similarity: 49.00% Conservative: 47
Best Local Similarity: 33.33% Mismatches: 105
Query Match: 13.12% Indels: 48
Gaps: 12
US-09-935-124a-1 (1-1422) x P2CA_HUMAN (1-382)
QY 417 GGTTCGAGGCGCTGATGCTGACCGGAGCGTGAAGGAGAGATGACAGATCCAC 476
DB 21 GYLeuHgrGlyGlyLeuSerSerMetGlnGlyTrpValGlnMetGlnSerPalaHis 40
QY 477 GTTCATCTGAGACATCAACCGAGAGGTGAGGCCCATGCTCCCTCATTACTGGGATT 536
DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeu--GlusertTrp 53
QY 537 TCATATTTTGGCTGTTTGGATGACATGAGAGAAATTCAGCCTCAAAATTTGTCACAG 596
DB 54 SerPhePheAlaValIleAspGlyHisAlaGlySerGlnValAlaIleValTyCysCysGln 73
QY 597 AATTGCAATCAAACTTATATCAAGAAATTTCTT---AAAGAGAT-----GTATCAGT 647
DB 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheIleGlySerAlaGlyAlaProSer 93
QY 648 GTAGAGAAACCGTAGAGAGATGCTTTGGACACCTTGAACATATACATGATGAAGATTC 707
DB 94 ValGln---AsnValIleAsnGlyIleArgThrGlyPheLeuGlnIleAspGlnHisMet 112
QY 708 CTTAAACAGCTTCACGACGACGCTCGTGAAGATGGGTTCACCTGACCTGGT 767
DB 113 ArgValMetSerGlnIleValSerHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
QY 768 CTGCTCTGACACAACTTTTATATGCGCACTGGAGATGTCGCGCAATCTGT 827
DB 133 LeuIleSerProGlnHisIleThrTyPheIleAsnIleCysGlyAspSerArgGlyLeuLeuCys 152
QY 828 CGTTATATGAGAGAGATCAAAACATGACGCTTAAAGCTTACGAAAGACATATCA 887
DB 153 Arg-----AsnArgValValHisPhePheThrGlnAspHisIleValPro 166
QY 888 ACTGATGATGAGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 947
DB 167 SerAsnProLeuGlnGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGln 186
QY 948 GTTTTGCGCTGCTGAGGTGTCAAGCTTCATTTGGGAGCGGCGAGTACAGCGCTGC--- 1004
DB 187 ValAsnGlySerLeuAlaValIleSerArgAlaLeuGlnIleAspPheAspTrpIle---CysVal 205
QY 1005 -----GATGTCACC-----TCGTGCGCGGACATGACA 1031
DB 206 HisGlyValGlyProThrGlnGlnIleValIleSerProGlnProGlnValHisAspIleGln 225
QY 1032 CGGTGCGAGCGTACCCCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1091
DB 226 ArgSerGln-----GlnAspArgPheIleHisIleLeuAlaCysAspGlyIleIleTrpAsp 243
QY 1092 GTCTTATCCCAAGAGAGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1145
DB 244 ValMetGlyAsnGlnIleLeuCysAspPheValArgSerArgGlnIleValIleThrAsp 263
QY 1146 AAGATTCAGACCCGGAAGGAGAAAGTCCGACGCGGCGCTTACGAGACGCTGCAAC 1205
DB 264 -----LeuGlnValValCysAsn 269
QY 1206 AGGCTGCGCAACAGAGCGGTGACGCGGCTGCGCGGACGACATGATGATGATGATGATGAT 1265
DB 270 GlnValValAspThrCysLeuTyIleGlySerArgAspAsnMetSerValIleLeuIle 289

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RESULT 13
P2C2_ARATH ID P2C2_ARATH STANDARD; PRT; 423 AA.
AC 004719;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C ABI2 (EC 3.1.3.16) (PP2C) (Abscisic acid-
inensitive 2).
GN ABI2 OR AT5G57050 OR MIM17.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta, and cv. Columbia;
RC MEDLINE=97308526; PubMed=9165752;
RX Leung J., Merlot S., Giraudat J.;
RA "The Arabidopsis ABSCISIC ACID-INSENSITIVE2 (ABI2) and ABI1 genes
RT encode homologous protein phosphatases 2C involved in abscisic acid
RL signal transduction.";
RL Plant Cell 9:759-771(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Landsberg erecta;
RC Rodriguez P.L., Grill E.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RC MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katch T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
CC -1- FUNCTION: INVOLVED IN ABSCISIC ACID (ABA) SIGNALING PATHWAY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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CC -----
DR EMBL; Y08966; CAA70163.1; -.
DR EMBL; Y08965; CAA70162.1; -.
DR EMBL; Y11840; CAA72538.1; -.
DR EMBL; AB024035; BAA97035.1; -.
DR HSSP; P35813; 1A6O.
DR InterPro; IPR001932; PP2C-1like.
DR InterPro; IPR00222; PP2C.
DR Pfam; PF00481; PP2C_1.
DR SMART; SM00331; PP2C_Sig.1.
DR SMART; SM00332; PP2Cg.1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydroxylase, Manganese, Manganese; Multigene family; Calcium-binding.
FT CA BIND 70
FT SEQUENCE 423 AA; 46306 MW; 670CACT6DAS51A171 CRC64;
Alignment Scores:
Pred. NO.: 1.78e-16 Length: 423
Score: 333.00 Matches: 118
Percent Similarity: 44.91% Conservative: 63
Best Local Similarity: 29.28% Mismatches: 130

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Query Match:	13.01%	Indels:	92
DB:	1	Gaps:	19
US-09-935-124A-1 (1-1422) x P2C2_ARATH (1-423)			
QY 252 CTCCACCCCGCTAGC--AGTGGCAGTTACAGT-----			281
Db 34 LeuProGluSerSerCySerSerGlyAlaMetLysAspSerSerPheGluLeuAn			53
QY 282 -----TCTCTTGCCACATCAATATCCACAGTGTAAACAGAGGAAAGGA			329
Db 54 ThrArgGlnAspSerLeuThrSerSerSerAlaMetAlaGlyValAsp----			70
QY 330 GCANAAGGAAAAACCTCCGAGAAAGAAAGATGCGAGGAAAGACTT-----			377
Db 71 -----IleSerAlaGlyAspGluLeuGlySerAspGluPheAspProArgSer			87
QY 378 -----GTGAAAAAGAAAGTTTGTA-----GCCTCTTGCGTATCTTGCTG			422
Db 88 MetAsnGlnSerGlnLysValLeuSerArgThrGluSerArgSerLeuPheGluPhe			107
QY 423 AAGGCGTAT-----GTGCGTGAACGGAAGGCTGAAGAGGAGAGATGCAAGAT			470
Db 108 LysCysValProLeuTyrGlyValThrSerIleCysGlyArgArgProGluMetCys			127
QY 471 -----GCCCAAGTCATCTGTGAACAC			491
Db 128 SerValSerThrIleProArgPheLeuGlnValSerSerSerSerLeuLeuAspGlyArg			147
QY 492 ATCACCAGAGGTGAGGCCCCCATCGTCCCTCATTAATCGGGTTCAATATTTGCTGT			551
Db 148 ValThrAsnGlyPheAspProIleAspSer-----AlaIlePhePheGlyVal			163
QY 552 TTGTGATGCAATGAGGAATTCAGAGCTCAAAATTTGCTGCACAGAAATTTGCAT			605
Db 164 TyrAspGlyIleGlyGlySerGlnValAlaLeuTyrCysArgGlnArgMetIleuAla			183
QY 606 -----CAAAACTTAATACGAAATATTTCTTAA-----GGAGATGTATACAGTGA			650
Db 184 LeuThrGlnGluLeuValLysGluLysProGluPheCysAspGlyAsp-----ThrTyr			201
QY 651 GAGAAAACCGTGAAGAGATGCTTTTGGACACTTTCAGACATATGATGAAGATTCTT			710
Db 202 GlnGluTyrTyrLysValAlaLeuPheAsnSerPheMetArgValAspSerGluLeu			221
QY 711 AAACAACTTCACGCCACAGAACTGCTGCGTGAAGAATGGTCCACGCCACGCTGTCTG			770
Db 222 ThrValAlaIleIleAspGluThrVal-----GlySerThrSerValAlaValAla			238
QY 771 GCTGTAGACAACATCTTTATTTATGCGCAACCTCGAGATAGTCGGGCATCTTGTCGT			830
Db 239 ValPheProThrIleIlePheValAlaLeuAspGlyValAspSerArgAlaValLeuCysArg			258
QY 831 TATATAGAGAGAGTCAAAAAACATGACGCTTAAAGCTTACGAAAGACATATCAACT			890
Db 259 -----GlyLysThrProLeuAlaLeuSerValAspHisLysProAsp			272
QY 891 CAGATAGAGAGCGGATGAGATACAGAAAGGCTGAGAGAAAGCT-----AGGAT			941
Db 273 ArgAspAspGluAlaAlaArgIleGluAlaAlaGlyLysValIleArgTrpAsnGly			292
QY 942 GAGCGGTGTTTGGCGCTGTAAGAGTGCACGCTCATTTGGGAGAGGAGACATCAAGGC			1001
Db 293 AlaArgValIlePheGlyValLeuAlaMetSerArgSerIleGlyAsp--ArgTyrLeuLys			311
QY 1002 TGCAGTGCCTCTGTGCCCAATCAAGACGTGCGACGTAAACCCCAATGACAGTTG			1061
Db 312 ProSerValIleProAspProGluValIleThrSerValArgArgValLysGluAspAspCys			331
QY 1062 ATTTGTTGGCGCTGTATGGGCGCTTCAAGGTCTTTAACCCCAAGAAAGCGGTGAATCT			1121
Db 332 LeuIleLeuAlaSerAspGlyLeuTyrAspValMetThrAsnGluGluValCysAspLeu			351


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Db      47 ProHLeuLeu---AspantPSePhePheAlaValTyrAspGlyHisAlaGlySer 65
QY      573 CGAGCTCAAAATTTGCTGCAAGATTTGCATCAAACTTA-----ATC 617
Db      66 ArgValAlaIaAspTyrCysSerThrHisLeuLeuGluHisIleThrThrAsnGluAspPhe 85
QY      618 AGAAAAATTCCTTAA---GGAGATGTATC-----AGTGTAGAGAAAACCGTGAAGAGA 668
Db      86 ArgAlaAlaAspTyrSerGlySerAlaLeuGluProSerValGlu---SerValTyrThr 104
QY      669 TGCCTTTTGACACTTTCAGCATCTAGATGAGATTCCTTAAACAGCTTCACCAAG 728
Db      105 GlyIleArgThrGlyPheLeuValIleAspGlyTyrMetArgAsnSerAspLeuArg 124
QY      729 AAGCCTGCTGGAAGATGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
Db      125 AsnGlyMetAspArgSerGlySerThrAlaValGlyValMetValSerProThrHisMet 144
QY      789 TATATTGCCAAGCTCGAGATAGTCCGGCAATCTTGTGTATATAGAGAGAGTCAA 848
Db      145 TyrPheIleAsnTyrGlySerAspArgAlaValIleuGlyAsnGlyGln----- 161
QY      849 AAGATGCAAGCTTAAAGCTCAGCAAGATCAATCAACTAGATATGAGAGCGGATG 908
Db      162 -----ValCyAspSerThrGlnAspHisGlySerProCyAsnProValGluValGlu 178
QY      909 AGGATACAGAGAGCTGAGAGAAAGTCAAGGATGAGGCTGTTGGCGGCTGAGAGGTG 968
Db      179 ArgIleGlnAsnHisGlySerValMetIleGlnHisGlyValAsnGlySerLeuAlaVal 198
QY      969 TCAGCTCATTTGGGAGCGGCGAGTCAAGACGCTGCGGT----- 1007
Db      199 SerArgAlaIleuGlyAspTyrAspTyrLysCyValAspGlySerProThrGluGln 218
QY      1008 ----GTACCTCTGTGCGCCATCAACAGCTGCGAGCTGACCCCAATGACAGTTCAAT 1064
Db      219 LeuValSerProGluProGluValTyrGluIleValAlaArgAlaGluGluAspGluPheVal 238
QY      1065 TTGTTGGCTGCTGATGGGCTCTTCAAGGCTTACCCCAAGAGACCGTGAACATTCATC 1124
Db      239 ValLeuAlaCysAspGlyIleThrAspValMetSerAsnGluIleuGlySerGluPheVal 258
QY      1125 TTGTCTGTCTCGAGATGAAAGATCCAGACCCGGGAAAGGAAAGTCCGACCGCAGCGC 1184
Db      259 LysSerArgLeuGlu-----ValSerAsp 266
QY      1185 CGCTACGAGACAGCTGCAACAGGCTGCCCAACAGCGGCTGACGGGCTTGCGCCGAC 1244
Db      267 AspLeuGluAsnValCysAsnThrValIleAspThrCysLeuHisGlySerArgAsp 286
QY      1245 AAGTCACTGTATGGTGGTG 1265
Db      287 AsnMetSerValValLeuVal 293

RESULT 15
P2CB RAT ID P2CB RAT STANDARD: PRT: 390 AA.
AC P35815: 064046:
DT 01-UN-1994 (Rel. 29, Created)
DT 01-UN-1994 (Rel. 29, Last sequence update)
DT 15-UN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (TA)
DE (Protein phosphatase 1B).
OS PM1B OR PPP1B OR PP2C2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Liver;
RX MEDLINE=92201367; PubMed=1312947;

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RA Wenk J., Trompeter H.-I., Pettrich K.-G., Cohen P.T.W., Campbell D.G.,
RA Mieskes G.;
RT "Molecular cloning and primary structure of a protein phosphatase 2C
RT isoform.";
RL FEBS Lett. 297:135-138(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=95169115; PubMed=7532404;
RA Schaefer K., Braun T.;
RT "Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg2+
RT dependent protein phosphatase beta.";
CC Biochem. Biophys. Res. Commun. 207:708-714(1995).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms, 1/Beta-1 (shown here)
CC and 2/Beta-MP; are produced by alternative splicing. Isoforms
CC appear to differ in their C-terminus.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: S90449; AAB21898.1; -.
DR EMBL: S74572; AAB33430.1; -.
DR PIR: S20392; S20392.
DR HSP: P35813; 1A60.
DR InterPro: IPR001932; PP2C-like.
DR InterPro: IPR000222; PP2C.
DR Pfam: PF00481; PP2C_1.
DR SMART: SM00331; PP2C_SIG; 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family;
KW Alternative splicing.
FT METRL 37
FT METRL 38
FT METRL 60
FT METRL 243
FT METRL 286
FT METRL 379
FT VARSPLIC 390
SQ SEQUENCE 390 AA; 42889 MW; D147615BC2FA140B CRC64;
ISOFORM 2).

Alignment Scores:
Pred. No.: 1.78e-15
Score: 319.00
Percent Similarity: 44.95%
Best Local Similarity: 29.36%
Query Match: 12.46%
DB: 1
Length: 390
Matches: 96
Conservative: 51
Mismatches: 124
Indels: 56
Gaps: 9

US-09-935-124A-1 (1-1422) x P2CB_RAT (1-390)
QY 333 AAGAGAAAACCTCGAGAGAGAGAGATGCGAGCTTGAGAGAAAGATT 392
Db 7 LysProLysThrGluLysHisAsnAlaHisGlyAlaGlyAsn----- 20
QY 393 TGTAAAGCTCTTCGATATCTTGTGCTGAAGGCTATGTGGCTGACGAGAGGTGAG 452
Db 21 -----GlyLeuArgTyrGlyLysSerSerMetGlnGlyTyr 32
QY 453 AGGAGAGATGACAGATGCCCATCTATCTGAAAGCATCAGAGAGATGTAGGCC 512
Db 33 ArgValGluMetGluAspAlaHisThrAlaValGlyIle----- 46

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OY 513 CCAATGCTCCATTAATCTGGGCTTCAATTTGCTTTTATGACATGAGGAAAT 572
DB 47 PCHISGLYLEU--GLAASPTSPSPHERPHEALALVALTYLAAASGLYSE 65
OY 573 CGAGCTCAAAATTTGCTGACAGAAATTTGATCAAAACTTA-----ATC 617
DB 66 ARGVALALASNTYRCYSESTHLEULEUUNHLEIETHTHRAENGLASRPH 85
OY 618 AGAAATTTCTTAAGAGATGATATC-----AGTGAAGAGAAAACGTGAAGCA 668
DB 86 ARGVALALASPLYSERGLYPHEALALEUGLUPROSERVALGLU---ASVALLYETH 104
OY 669 TGCCCTTTGACACATTTGACATATCATGATGAAGAGTCTTAACACGCTTCACGAC 728
DB 105 GLYLLEARGTHGLYPHEALTYLLEASPSGLUTYMETARGASPHSEARPLEAUG 124
OY 729 AAGCTGCTGGAAGAGGTCACGTCGACGCTGTCTGTGCTGTGATGACATATCTT 788
DB 125 AENGLYMETASPARISERGLYSETHRALVALGLYVALMETILLESERPROTHHISLE 144
OY 789 TATATTGCCAAGCTGAGATATGTCGGGCAATCTGTGCTGCTTATATGAGAGAGTCA 848
DB 145 TYRPHLEIENCYSELVASESERHVALLEVALLECYAAYASNGLYGLN----- 161
OY 849 AAACATGACGCTTAAGCTGACGAAAGACATATTCACATCACTAGATGAAGCGGAT 908
DB 162 -----VALCYPHESETHNGHASPHEILYSPFCYASNPROMETGLULYGLU 178
OY 909 AGGATTCAGAGGCTGAGAGAAACGTGACGAGTGGCTTTTGGGCTCTAGAGCTG 968
DB 179 ARGILEGLIASHLAGLYGLYSERVALMETILEGLIARXVALASNGLYSERLEUALA 198
OY 969 TCAAGCTCAATGGGAGCGGACATPACAGCGCTGGCT----- 1007
DB 199 SEVALGALALEUGLYASRYLYASRYLYLVSUYALASRYLYVAGLYPROTHGLUGL 218
OY 1008 ---GTACCTCTGTGCCCCACATCAGACGCTGACAGTACCCCAATGACAGGTTGAT 1064
DB 219 LEVALISERPROGLUPROGLIIVALTYLGLIILEUALAGLIGLILASRGLUPRHE 238
OY 1065 TTGTGCTGCTGATGGGCTCTCAAGCTCTTACCCAGAGAGAGAGCGGTAACTTAT 1124
DB 239 VALLEUALICYAASRGLYILETRPVARVALMETSEARASNGLIGLILEUCYGLUPRHE 258
OY 1125 TTGTCTGCTGAGAGTGAAGAAAGATCCAGACCCGGAGAGGAGAGTCCGACGCG 1184
DB 259 ASNSERARXGLEUGLU-----VALSERARP 266
OY 1185 CGGTAGAGAGAGAGCTGACAGAGCTGCGGACAGAGGCGGTGACGCGGCGGAC 1244
DB 267 ASRLEUGLIASNTVALCYAASNTTPVALVALASRTHCYULENHILEYGLYSETR 286
OY 1245 AAGCTCACTGATGCTGCTG 1265
DB 287 ASHMETSEFILLEVALLEUAL 293

RESULT 16
P2C1_YEAST STANDARD: PRT; 281 AA.
AC P3182;
DT 01-FEB-1994 (rel. 28, Created)
DT 01-FEB-1994 (rel. 28, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE Protein phosphatase 2C homolog 1 (BC 3.1.3.16) (PP2C-1).
GN P2C1 OR TPDI OR YDL006W OR D2925.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93360976; PubMed=8395005;

```

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RA Maeda T., Tsai A.Y.M., Saito H.;
RT "Mutations in a protein tyrosine phosphatase gene (PTP2) and a
RT protein serine/threonine phosphatase gene (P2C1) cause a synthetic
RT growth defect in Saccharomyces cerevisiae."
RL Mol. Cell. Biol. 13:5408-5417(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94254822; PubMed=8196609;
RA Robinson M.K., van Zyl W.H., Philbrick E.M., Broach J.R.;
RA "TPD1 of Saccharomyces cerevisiae encodes a protein phosphatase
RT 2C-like activity implicated in tRNA splicing and cell separation."
RL Mol. Cell. Biol. 14:3634-3645(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=528bc;
RA Andre B., Vissers S., Urrestarazu L.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 167-281 FROM N.A.
RC STRAIN=528bc / AB972;
RA Murphy L., Richards C., Gentles S., Harris D., Barrell B.G.;
RA Rajadream M.A.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IT HAS A SERINE AND A WEAK TYROSINE PHOSPHATASE ACTIVITY
CC WITH RATIOS OF SERINE TO TYROSINE PHOSPHATASE ACTIVITY AS HIGH AS
CC 200:1. IT IS ESSENTIAL FOR GROWTH OR GERMINATION AT 37 DEGREES
CC CELSIUS. MAY HAVE A ROLE IN THE HEAT SHOCK RESPONSE. INVOLVED IN
CC RNA SPLICING AND CELL SEPARATION.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS. MANGANESE IS
CC ABOUT 20 TIMES MORE EFFICIENT THAN MAGNESIUM.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; L14593; AAA34920.1; -.
DR EMBL; Z48432; CAAB8353.1; -.
DR EMBL; Z74054; CAAB8552.1; -.
DR EMBL; Z48008; CAAB8055.1; -.
DR PIR; S41854; S41854.
DR HSSP; P35813; 1A60.
DR SGD; S0002164; P2C1.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR002222; PP2C.
DR Pfam; PF00481; P2C 1.
DR SMART; SM00321; P2C Sig. 1.
DR SMART; SM00321; P2C 1.
DR PROSITE; PS01032; P2C; 1.
KM Hydroxylase; Magnesium; Manganese; Multigene family; Heat shock.
FT METAL 36
FT METAL 37
FT METAL 38
FT METAL 58
FT METAL 233
FT METAL 272
FT METAL 272
FT CONFLICT 53
FT CONFLICT 124
FT CONFLICT 124
SQ SEQUENCE 281 AA; 31549 MW; FA384D2541B20D50 CRC64;

Alignment Scores:
Pred. No.: 2,11e-15
Score: 317.50
Percent Similarity: 45.87%
Best Local Similarity: 31.35%
Query Match: 12.40%
DB: 1
Gaps: 12
Length: 281
Matches: 95
Conservative: 44
Mismatch: 93
Indels: 71

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US-09-935-124A-1 (1-1422) x P2C1_YEAST (1-281)
QY 432 GTGGCTGAGCGGAGGAGTGA-----AGGAGAGAGATGCAAGATGCCACGTCATCTTG 485
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 23 ValAlAGLunbnybAnSerLySpheArXgThMeclunbValhIsthrYVal 42
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 486 AACGACATCAACGAGAGGTAGCCCCCGCTGCTCTTACTTCTGGGTT-----TCA 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 43 LysAenPheAla-----SerArgLeuAptirpGly 52
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 540 TATTTTGCTGTTTGTGATGAGATTCGAGCCTCAAAATTTGTCGACAGATT 599
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 53 TyrPheAlaValbPheApGlyhIbAlaGlyIleGlnhIAserYstrpCybGlybShIs 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 600 TTGCAT-----CAAACTTAATCAGAAAATTTCTTAAGAGATGTAACTAGT 647
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 LeuHieThrlerIleGlnhIAsenIleLeu-----AlaAp 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 648 GTRAGAAAAACGTGAAGAGATGCTTTTGACACTTTCAGACATCTGTAAGGTTG 707
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 GluThrArgAspValArgAspValLeuAsnAspSerPheLeuAlaIleApGlnGluIle 104
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 708 CTTAAACAAGCTTCCAGACGCTGCTGAAAGATGGTCCACT--GCCAGGTG 764
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 -----AenThrLybLeuValGlybAsnSerGlyCsthrAlaAlaValCys 119
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 765 GTTCTG-----GCTGTAGACAACATT-----785
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 ValLeuArgTrpGluLeuProAspSerValSerAspAspSerMetAlaGlnhIs 139
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 786 -----CTTATATATGCAACCTCGAGAGATAGTCGGGCACTTGTGTCTTAAAT 836
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 140 GlnArgLybLeuYrThrAlaAsnValGlyAspSerArGlyIleValLeuPheArgAnGly 159
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 837 GAGGAGAGTCAAAAACATGACGCTTAAGCTGAGAAAGATATCAACATCACTAGT 896
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 160 Aen-----SerIleArgLeuThrYrAspHlybAlaSerAspThr 173
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 897 GAAGACCGATGATACAGAAAGCTGAGAAACGTCAAGGATGGCGTGTGTTGGG 956
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 174 LeuGlnMetGlnArgValGlnGlnhIAsnGlyGlyLeuIleLeuLybSerArGValAnGly 193
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 957 GTCTGAGAGGTGTCAGGCTTCATTGGGAGCGGACATCAAGCGTGGCTGCACCTCT 1016
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 194 MetLeuAlaValhIAsrYserIleuGlyAspLybPhePheSerIleuValIleGlySer 213
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1017 GTGCCGACATCAAGCGCTCCAGTCCGACCCCAATGACAGTTCATTTGTGGCTGT 1076
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 214 ---ProPheThrYrSerValGlnIlehIAsnSerGlnAspLybPheLeuIleLeuAlaCys 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1077 GATGGCTCTTCAAGGCTTTTACCAGAGAAAGCCGTGAACCTTCACTTGTCTGTCTC 1136
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 233 AspGlyLeuTrpAspValIleAspArgGlnAspAlaCysGlnLeuIleLybAspIleThr 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1137 GAGGATGAAAAATCCAGACCCGGAAGGAGAACTCCGACCCGACCCGCTACGAAGA 1196
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 253 GluProAsnGlu-----256
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1197 GCCTGCAACAGCTGGGCAACAGAGCGGTGACGGGGCTCGGCGACACATCACTGTG 1256
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 AlaAlaLybValLeuValArgTyAlaLeuGlnAnGlyThrAspAsnValThrVal 276
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1257 ATGGTGGTG 1265
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 MetValVal 279
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta).
GN PPM1B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OK NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=98146173; PubMed=9486768;
RA Klump P.S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;
RT "Protein phosphatase type-2C isozymes present in vertebrate retinae:
RT purification, characterization, and localization in photoreceptors.";
RL J. Neurosci. Res. 51:328-338(1998).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate. BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL, AJ005458; CA006555.1; -.
DR HSP, P35813; IAOQ.
DR InterPro; IPR001932; PP2C-1like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C_1.
DR SMART, SM00331; PP2C-SIG; 1.
DR SMART, SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family.
FT MERTL 37 37 MANGANESE 1 (BY SIMILARITY).
FT MERTL 38 38 MANGANESE 1 (BY SIMILARITY).
FT MERTL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT MERTL 243 243 MANGANESE 2 (BY SIMILARITY).
FT MERTL 286 286 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 387 AA; 42834 MW; D70B95141250FFB1 CRC64;

Alignment Scores:
Pred. No.: 4.07e-15 Length: 387
Score: 314.00 Matches: 95
Percent Similarity: 44.65% Conservative: 51
Best Local Similarity: 29.05% Mismatches: 125
Query Match: 12.27% Indels: 56
DB: 1 Gaps: 9

US-09-935-124A-1 (1-1422) x P2CB_BOVIN (1-387)
QY 333 AAGAGAAAAACCTCCGAGAGAGAGATGCGACGTGAGAGCTTGTGAAAAGAAAGTT 392
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 7 LysbProLybThbGlnbLynhIAsnAlaIleGlyAlaGlyAen-----20
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 333 TGTAAAGCCTTCCGATATCTTGTGTTGAAGGCTATGTGGCTGACCGGAAAGGTGAG 452
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 -----GlyLeuArgTyArgLyLeuSerSerMetGlnIleYTrp 32
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 453 AGGAGAGATGACAGATGCCACATCTCGAAGCAATCACCGAGAGATGAGGCC 512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 ArgValGlnMetGlnAspAlaIleThrAlaValAlaGlyIle-----46
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 513 CCAATGCTCCATATACGCGGCTTCATATATTTGCTGTTTGTATGATGACGAGAAAT 572
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 ProhIseGlyLeu---GluAspTrpSerPhePheAlaValIlyrAspGlyhIleAlaGlySer 65
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 573 CGAGCTCAAAATTTGTCGACAGAAATTTGCATCAAAAATTAATCAGAAA-----623

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Db 66 ArgValAlaAsnTyrCysSerThrHisLeuLeuGluHisLeuTyrAsnAsnGluAspPhe 85
Qy 624 -----TTTCCTAAAGAGAGATGTAATC-----AGTGAAGAGAAACCGTGAAGAGA 668
Db 86 ArgAlaAlaGlyLysSerGlySerAlaLeuGluProSerValGlu---AsnValLysAsn 104
Qy 669 TGCCTTTTGACACTTTCACACATCATCATGTAAGAGAGTTCCTTAAACAGCTCCACGAG 728
Db 105 GlyTLeArgThrGlyPheLeuLysIleLeuArgLysTyrMetArgAsnPhnSerAspLeuArg 124
Qy 729 AAGCGTCGCTGGAAGAGAGTCCACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 788
Db 125 AasnGlyMetAspArgSerGlySerThrAlaValAlaGlyValMetIleSerProLysIle 144
Qy 789 TATATTGCCAAGCTGCAAGATAGTGGGCAATTTGTGCTTATATAGAGAGAGTCAA 848
Db 145 TyrPheIleAsnGlyAspSerArgAlaValLeuTyrArgSerGlyGln-----161
Qy 849 AAGATGACGCTTAAGCTCAGCAAGAGACATATCCAACTCAGTATGAAGCGGATG 908
Db 162 -----ValCysPheSerThrGlnAspHisLysProCysAsnProArgGluLysGlu 178
Qy 909 AAGATACAGAAAGCTGAGAGAAAGCTCAGGATGGCGCTGTTTGGCGTGTAGAGTGT 968
Db 179 ArgIleGlnAsnAlaGlyLysSerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
Qy 969 TCACGCTCATTGGGAGCGGCGAGTACAGCGCTGCGGT-----1007
Db 199 SerArgAlaLeuGlyAspTyrAspTyrLysCysValAspGlyLysGlyProThrGluGln 218
Qy 1008 ---GTACCTCTGTGCGCAGATCAGACGCTGCAGCTGACCCCAATGACAGGTTTCAAT 1064
Db 219 LeuValSerProGluProGluValTyrGluIleLeuArgAlaGluGluAspGluPheIle 238
Qy 1065 TTGTTGGCGCTGATGGCTCTTCAGAGCTTTTACCCAGAAAGCGGTGACTTCATC 1124
Db 239 IleLeuAlaCysAspGlyIleTyrAspValMetSerAsnGluGluLeuGlySerVal 258
Qy 1125 TTGTCTGTCTTCAGAGATGAAAGATCCAGACCCGGGAAAGGAAAGTCCGACCGACGCC 1184
Db 259 LysSerArgLeuGlu-----ValSerAsp 266
Qy 1185 CGGTACGAAAGAGCTGCAACAGCTGGCCACAGACGCGGTGACGGCGCTGGCCGAC 1244
Db 267 AspLeuGluAsnValCysAsnTyrPValAlaAspThrCysLeuHisLysGlySerArgAsp 286
Qy 1245 AAGCTCAGTGTGATGCTGTG 1265
Db 287 AsnMetSerIleValLeuVal 293

RESULT 18
P2CB_HUMAN STANDARD; PRT; 479 AA.
AC 075688; OS:HAVR;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta).
GN PPM1B OR PP2CB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM BETA-1).
RX TISSUE=Liver;
RX MEDLINE=98348020; PubMed=9694878;
RX Murely A.E., Kline A., Crabtree G., Sullivan J.B., Bert R.K.,
RX The cloning, expression and tissue distribution of human PP2Cbeta.",
RX FEBS Lett. 431:121-124(1998).
RP [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA-2).

Rx PubMed=10945995;
Ra Cheng A., Kaidis P., Solomon M.U.;
Rt "Dephosphorylation of human cyclin-dependent kinases by protein
Rt phosphatase type 2Calpha and betac2 isoforms.";
Rt J. Biol. Chem. 275:34744-34749(2000).
Rn [3]
Rp SEQUENCE FROM N.A. (ISOFORMS BETA-1 AND BETA-2).
Ra Sequenci E., Shani N., Hayut A., Falser S., Ben-Meir D., Divianki I.,
Ra Smorodinsky N.I., Lavi S.;
Rt "Protein phosphatase 1B. Cloning and characterization of two major
Rt transcripts generated by alternative use of 3' exons.";
Rt Submitted (FEB-2000) to the EMBL/GenBank/DBD databases.
Rn [4]
Rp SEQUENCE FROM N.A. (ISOFORM BETA-2).
Rc TISSUE=Adrenal gland;
Ra Peng Y., Gu Y., Li Y., Fu S., Gu J., Zhang L., Jiang C., Yu Y.,
Ra Han Z., Wang Y., Chen Z., Fu G.;
Rt "A novel gene expressed in human adrenal gland.";
Rt Submitted (JAN-2001) to the EMBL/GenBank/DBD databases.
Cc -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY. DEPHOSPHORYLATES CDK2
Cc AND CDK6 IN VITRO.
Cc -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
Cc phosphate.
Cc -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
Cc -1- SUBUNIT: MONOMER (BY SIMILARITY).
Cc -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; Beta-1/Beta-X/PPM1B2
Cc (shown here) and Beta-2/PPM1B1, are produced by alternative
Cc splicing.
Cc -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND SKELETAL MUSCLE.
Cc -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
Cc -----
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Cc use by non-profit institutions as long as its content is in no way
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Cc or send an email to license@ebi.ac.uk).
Cc -----
DR EMBL, A005801; CAA06704.1; -
DR EMBL, AF294792; AAG02232.1; -
DR EMBL, AJ271832; CAC27992.1; -
DR EMBL, AJ271835; CAC27992.1; -
DR EMBL, AF136972; AAG49433.1; -
DR HSSP, P35813; 1A60.
DR Genew; HGNC:9276; PPM1B.
DR MIM, 603770; -.
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolyase; Magnesium; Manganese; Multigene family;
KW Alternative splicing.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).
FT METAL 286 286 MANGANESE 2 (BY SIMILARITY).
FT VARSPPLIC 379 387 ASDEAREBSG -> GAGDELEPW (IN ISOFORM BETA-
FT 2)
FT VARSPPLIC 388 479 MISSING (IN ISOFORM BETA-2).
SQ SEQUENCE 479 AA, 52642 MW, A3A579AD263DBD CRC64;

Alignment Scores:
Pred. No.: 5,06e-15 Length: 479
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
DB: 1 Gaps: 8

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[illegible]

AC P40371.1
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 1 (EC 3.1.3.16) (PP2C-1).
GN PTC1 OR SPCCAFL1.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=972;
RC MEDLINE=94254832; PubMed=8196617;
RA Shiozaki K., Akhavan-Niaki H., McGowan C.H., Russell P.;
RT "Protein phosphatase 2C, encoded by ptc1+, is important in the heat
RT shock response of Schizosaccharomyces pombe.";
RT Mol. Cell. Biol. 14:3742-3751(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC MEDLINE=972;
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris B., Hidalgo J., Hodgson G.,
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odel C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Voickart G., Aert R., Robben J., Gymnopoulos B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Wambut R., Punelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaurie V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakowski G.V., Usarey D., Barrall B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -1- FUNCTION: IT HAS A SERINE AND THREONINE PHOSPHATASE ACTIVITY.
CC HAS A SPECIALIZED ROLE IN THE HEAT SHOCK RESPONSE. MAY BE
CC RESPONSIBLE FOR THE DEPHOSPHORYLATION OF HSP90. ALSO HAS A ROLE
CC IN MAINTAINING OSMOTIC STABILITY.
CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H2O = a protein +
CC phosphate.
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
CC EMBL; L26970; AAA35327.1; -;
DR EMBL; AL117389; CAB55768.1; -;
DR HSPB; P35813; IAG0
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.

DR SMART; SM00311, PP2C SIG; 1.
DR SMART; SM00312, PP2C; 1.
DR PROSITE; PS01032, PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family; Heat shock.
SQ SEQUENCE 347 AA; 38676 MW; 506754545502403B CRC64;

Alignment Scores:

Pred. No.:	1-se-14	Length:	347
Score:	306.00	Matches:	101
Percent Similarity:	43.99%	Conservative:	60
Best Local Similarity:	27.60%	Mismatches:	129
Query Match:	11.95%	Indels:	76
DB:	1	Gaps:	14

US-09-935-124A-1 (1-1422) x PP2C1_SCHPO (1-347)

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QY 264 AGCAGTGGCGATTCAGGTTCTCTTGGCAGCATATGCCAGATGTAAAGACTGAAGG 323
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    4 SerHisProMetAlaGlySerLeuLeuGluProLeuHisIleValu-----Aan 19

QY 324 AAGAGCAAGAAAGAAAACCTCCGAGAGAAAGATGGCATGAAG----- 374
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    20 ProPheSerGluAenSerHisSerGlyHisArgIlySerAlaSerAspHisSerAlaAsp 39

QY 375 -----CTTGGCAAAAGAAAGTTGTAAAGCTTTCGGTGATCTTT 416
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    40 GlyIuThrArgProIleAlaIleGluMetIlyAspSerIlyGlyAenThrValProVal 59

QY 417 GGT-----CTGAAGGCTTATGTGGTGAAGCGGAAG 446
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    60 GlyAenSerArgProSerIlyValAspAenThrLeuAlaGlyLeuMetGluAepIlyAen 79

QY 447 GGTGAG--AGGAGAGATGACAGATGCCACGTCACTCTGAACGACATCACCGGAG 503
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    80 GluArgTrpArgArgSerMetGluAepThrHisIleCysLeuThrArgAspPheGlyAen 99

QY 504 TGTAGGCCCATCGTCCCTCATTAATCCGGGTTTCATTTGTGGTGTGTGAATGACAT 563
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    100 -----GluAepArgGlyPheValAlaValIlyArgAspGlyHis 111

QY 564 GGAGGATTCGAGCCTCAAAATTTGGTGGCAGATTTTGTCAAACTTAATCAAGAAA 623
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    112 AlaGlyIleGlnAlaSerAspIlyArgGlnIlySerAlaGlnIlyValLeuLeuGlnIly 131

QY 624 TTTCTAAGAGAGATGTATCAGTGTAGAGAAACCGTGAAGAGATGCCCTTTGGACACT 683
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    132 -----ValArgAenGluProAepArgIlyLeuValIthrAspLeu 143

QY 684 TTCAAGCATCTGATGAAAGATTCTTAAACAAGCTTCCAGC--CAAGAGCTGCCTGG 740
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    144 Met-----AspGluThrPheValIgluValAenSerIlyIleAlaIlyAlaThrHis 160

QY 741 AAAGTGGGTCCACTGCCAGGTGTGTGGCT-----GTA 776
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    161 AenAspIleCysGlyCysThrAlaAlaValAlaPheAspArgIlyArgIlyAspArgThr 180

QY 777 GACAACTTTCTTTATTTATTCGCACTCGAGATAGTCGGGCAATCTTGTGCTTATAT 836
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    181 ArgArgValIleuIlyThrAlaAlaAlaGlyAspAlaAlaGlyIleValLeuCysAspArgIly 200

QY 837 GAGGAGAGTCAAAAACATGACGCTTAAGCTCTAGCAAAAGCATTAATCCAACTAGTAT 896
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    201 Iys-----AlaIleArgLeuSerIlyAspHisIlyGlySerAspAla 214

QY 897 GAAGAGCGGATGAGATACAGAAAGCTCGAGAGAAAGCTGACGAGATGGCGTGTATTGGGC 956
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    215 AenGluSerArgValIthrGlnLeuGlyIlyLeuMetValIgluAenArgIleAenGly 234

QY 957 GTGTAGAGGTGTCAAGCTCATTTGGGAGCGGAGCATGTAACAAGCCTCGGTGCACCTCT 1016
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    235 ValLeuAlaValIthrArgAlaLeuGlyAspThrIlyIlyLeuIlyGlnLeu---ValSerAla 253

QY 1017 GTGCCGAGATCAGACGCTGCACAGCTG--ACCCCAATGACAGATTCAATTTGTGGCC 1073

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DB 254 HisProPheThrThrGluThrArgIleTrpAsnGlyHisAspGluPhePheIleAla 273
QY 1074 TGTGATGGCTCTCTCAAGATCTTTTACCCCAAGAAAGCGGTGAACCTTATCTTCTGT 1133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    274 CysAspGlyLeuThrArgValValSerAspGlnGluAlaValAspPheValArgAspPhe 293
QY 1134 CTCGAGAGTGAAGAAATCCAGACCCGGAGAGGAGAGTCCGACGCCGCTTACGAA 1193
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    294 -----ValSerProArgIlu----- 298
QY 1194 GCAGCTTCGACAGGCTGCCCAACAGAGCGGTGACAGCGGCTCGACCAACATGACT 1253
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    299 ---AlaIleValArgLeuValGluPheAlaIleuIlyArgLeuSerThrAspAsnIleThr 317
QY 1254 GTATGTTGTGTGGGATA 1271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
    318 CysIleValValAsnLeu 323

RESULT: 20
PP2C_YEAST STANDARD; PRT; 464 AA.
AC P39366;
DT 01-FEB-1995 (rel. 31, Created)
DT 01-FEB-1995 (rel. 31, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE Protein phosphatase 2C homolog 2 (Pc 3.1.3.16) (PP2C-2).
GN PTC2 OR YER089C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetaceae; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP Maeda T., Teal A.Y.M., Saito H.;
RA Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=5289C / AB972;
RA Dietrich P.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Becro A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Honicke-Smith S.,
RA Hyman R., Kayser A., Kemp C., Lashkari D., Lew H., Lin D.,
RA Moseedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petrel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.M.,
RA Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RL [3]
RN FUNCTION.
RP PubMed=10580002;
RX Cheng A., Ross K.E., Kaldis P., Solomon M.J.;
RT "Dephosphorylation of cyclin-dependent kinases by type 2C protein
RT phosphatases."
RL Genes Dev. 13:2946-2957(1999).
CC -!- FUNCTION: Responsible, together with PTC3, for the
CC dephosphorylation of the cyclin-dependent protein kinase CDC28.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL; U18839; AB964644.1; -
DR EMBL; U12498; AB017392.1; -
DR HSRP; P35813; 1A60.
DR SDB; S0000891; PTC2.

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RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Bedhia N., Gnoj L., Schutz K., Huang B., Spiegel L.,
 RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Thieleh J.,
 RA Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Lestrille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton L., Mardis E., Miller N., Greco T., Kemp K.,
 RA Kramar J., Fulton L., Mardis E., Danne M., Pepin K., Hillier L.,
 RA Nelson J., Spierth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berchhoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston P., Vil D., Shether M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
 RA Grant S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
 RA Chen E., Maria W., Mathiesen R., McCombie W.R.,
 RA Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana. "769-777(1999).
 RL Nature 402:769-777(1999).
 CC -i- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -i- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -i- SIMILARITY: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
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 CC -----
 DR EMBL; U34803; AAA92889.1; -.
 DR EMBL; AL161571; CAB81429.1; -.
 DR EMBL; AL078579; CAB43668.1; ALT_SEQ.
 DR InterPro: IPR001932; PP2C-like.
 DR InterPro: IPR000222; PP2C.
 DR Pfam: PF00481; PP2C.
 DR SMART; SM00331; PP2C_Sig; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 DR Hydrobase; Magnesium; Manganese; Multigene family.
 KM METAL 93 93 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 296 296 MANGANESE 2 (BY SIMILARITY).
 FT METAL 326 326 MANGANESE 2 (BY SIMILARITY).
 FT CONFLICT 1 4 MALL -> SNSS (IN REF. 2).
 FT CONFLICT 69 70 RD -> QY (IN REF. 2).
 FT CONFLICT 271 271 D -> N (IN REF. 2).
 FT CONFLICT 353 353 W -> C (IN REF. 2).
 FT CONFLICT 360 388 RQNVVVELVQAATTTGIVTGVIMMSHLS -> TKRSG
 (IN REF. 2).
 SQ SEQUENCE 388 AA; 42719 MW; 4956CCCT86AEB802 CRC64;
 Alignment Scores:
 Pred. No.: 1.81e-14 Length: 388
 Score: 305.00 Matches: 87
 Percent Similarity: 47.34% Conservative: 64
 Best local Similarity: 27.27% Mismatches: 102
 Query Match: 11.81% Indels: 66
 DB: 1 Gaps: 11
 US-09-935-124a-1 (1-1422) x P2C3_ARATH (1-388)
 QY 426 GCGTATGCGCTGACGGAGGCTGAGAGAGATGAGATGCCAGCTGATCTTG 485
 DB 61 GYLYTThrSerVal---GIndGlyPheArgAspGluMetGluAspAspIleValIleArg 79
 QY 486 AACGACATCCAGCAGAGAGTGAAGCCCCCATGCTCCCTCATTAATCGGGTTTCATATTTT 545
 DB 80 SerAspAlaValAspSer-----PheSerTyrAla 89
 QY 546 GCTGTTTTCATGACATGACGATTCGAGCTCAAAATTTTCGACAGATTCGAT 605
 DB 90 AlavalPheAspGlyVHIsalaglySerSerSerValIlyPheIleuArgIleuLeuArg 109

QY 606 CAAACTTAATCACAAAATTTCTTAAGAGATGATATCATGCTGAG-AAAACC 659
 DB 110 LysGluCysValAlaIleValLeuGlnIleValSerLeuLeuSerValIleValPheAlaIle 129
 QY 660 GTGAAGAGATGAGCTTTTGGACCTTTCAGACATCTCATGATGAAGTCTCTTAA----- 713
 DB 130 IleValGlnAlaLeuIleValLeuValAlaPheGluSerValAlaPheArgSerLeuLeuSerPhe 149
 QY 714 CAAGCTTCAGCCAGAGCTGCTCGAAGAGATGAGTCCAGCTGCGACGCTGCTGAGCT 773
 DB 150 GluValAlaSerValIleValIleValIleValIleValIleValIleValIleValIle 168
 QY 774 GTAACCAACATTTCTTATATTTCCCACTCGCATATGCTGGCATCTTGTGCTTAT 833
 DB 169 ArgSerAspValSerPheIleAlaIleIleValIleValIleValIleValIleValIle 188
 QY 834 AATGAGAGAGTCAAAAACATGACCTTAAGCTTGAACCAAGCATATCA----- 887
 DB 189 GlyIleIleGluIle-----LeuThrAspTyrHisArgProTyrGly 202
 QY 888 -----ACTGATGATGAGAGCGAGTACGATACGAGAGCTGAGAAACCTCAG 938
 DB 203 SerSerArgAlaIleAlaIleIleGlnIleValIleValIleValIleValIleValIle 222
 QY 939 GATGGCGGTGTTTGGCGCTGCTAGAGGTGTCAGCTTCATGCGAGCGGACATACAG 998
 DB 223 AsnGlyArgIleCysGlyAspIleAlaValSerArgAlaPheGlyAspIleArgPheIys 242
 QY 999 -----CGTGGCGT----- 1007
 DB 243 ThrIleValSerAspMetLeuIleValIleValIleValIleValIleValIleValIle 262
 QY 1008 -----GTCACTCTGCGCCAGCATACAGAGCGTC 1037
 DB 263 ValSerArgIleGluIleValIleValIleValIleValIleValIleValIleValIle 282
 QY 1038 CAGCTGACCCCATGACAGCTTCATTTTGGCTCTGATAGGCTCTTCAAGTCTTT 1097
 DB 283 ProLeuThrSerArgPheValGluIleIleValIleValIleValIleValIleValIle 302
 QY 1098 ACCCCAGAGAGACCGTGAACCTTCATCTTCTGCTCGAGATGAAAAGATCCAGACC 1157
 DB 303 LysSerSerArgPheValIleValIleValIleValIleValIleValIleValIle 315
 QY 1158 CGGAGAGGAGAGTCCGACCGACCGCTGACGAGACGCTGCAACAGCTGAGCCCAAC 1217
 DB 316 ArgIys-----HisGlyValSerValIleValIleValIleValIleValIleValIle 330
 QY 1218 AAGCGGAGCGAGCGGCTCGGCCGACAGCTCACTGATGAGGTGGTGGATAGG 1274
 DB 331 ValAlaLeuSerPheArgSerGlnSerGlnSerIleIleIleAlaSerPheGly 349
 RESULT 22
 P2C1_CABE1. STANDARD; PRT: 491 AA.
 AC P49585.
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Probable protein phosphatase 2C P4269.1 (EC 3.1.3.16) (PP2C).
 GN P4269.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 ON NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Tatch A., Waterston R.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -i- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.

RA Maeda T., MurJger-Murphy S.M., Saito H.;
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 RN (3)
 RF FUNCTION.
 RX PubMed=10580002;
 RA Cheng A., Rose K.E., Kaldis P., Solomon M.J.;
 RT "Dephosphorylation of cyclin-dependent kinases by type 2C protein
 phosphatases.";
 RL Genes Dev. 13:2946-2957(1999).
 CC -1- FUNCTION: Responsible, together with PTC2, for the
 dephosphorylation of the cyclin-dependent protein kinase CDC28.
 CC -1- CATALYTIC ACTIVITY: A phosphoprotein + H(2O) = a protein +
 phosphate.
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE PTC2 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

DR EMBL; Z23261; CA480791.1; -;
 DR EMBL; Z35817; CA484876.1; -;
 DR EMBL; U72346; AAB17351.1; -;
 DR PIR; S39832; S39832.
 DR PIR; S37333; S37333.
 DR HSSP; P35813; 1A6Q.
 DR SGD; S0000152; PTC3.
 DR InterPro; IPR001932; PTC2-like.
 DR InterPro; IPR000222; PTC2.
 DR Pfam; PF00481; PTC2_1.
 DR SMART; SM00331; PTC2_SIG; 1.
 DR PROSITE; PS01032; PTC2G; 1.
 DR PROSITE; PS01032; PTC2G; 1.
 KM Hydrolyase; Magnesium; Manganese; Multigene family.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 62 62 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 234 234 MANGANESE 2 (BY SIMILARITY).
 FT METAL 284 284 MANGANESE 2 (BY SIMILARITY).
 FT CONFLICT 369 369 D -> G (IN REF. 2).
 SQ SEQUENCE 468 AA; 51390 MW; DC5C18053828DCDD CRC64;

Alignment Scores:
 Pred. No.: 2.7e-13 Length: 468
 Score: 289.00 Matches: 93
 Percent Similarity: 46.44% Conservative: 57
 Best Local Similarity: 28.79% Mismatches: 117
 Query Match: 11.29% Indels: 56
 DB: 1 Gaps: 14

US-09-935-124a-1 (1-1422) x PTC3_YEAST (1-468)

QY 366 AGTGAAGAGCTGTGGAAGAAGCTTGTAAAGCCTCTTCGGTATC-----TTTGGT 419
 Db 6 SerAsnProIleIleAspLysGlnHisSerGlyThrAspCysLeuThrAlaPheGly 25
 QY 420 CTGAAGGCTATGTGGCTGACCGAAGGCTGAAGGAGAGAGATGACAGATGCCACGTC 479
 Db 26 Ieu-----CysAlaMetGlnGlyTPrAspMetSerMetGlnAspAlaHisIle 41
 QY 480 ATCTGAACGACATCACCAGAGAGCTGAGGCCCCCATGCTCCCTCATTAATTCGGGGTTCA 539
 Db 42 ValGluProAsnLeuLeuAlaGlu-----SerAspGluGlnHisIleAla 56
 QY 540 TATTTGCTGTTTGTGATGACATGAGGAATTCAGCCTCAAAATTTGCTGCACGAGAT 599
 Db 57 PheTyrGlyIlePheAspGlyHisGlyIleGlySerSerValAlaGluPheCysGlySerLys 76
 QY 600 TTGCATCAAACTAATCAGAAA-----TTCTTAAGGAGATGATCATGATGATGAG 653

Db 77 MetIleSerIleLeuLysLysGlnIleuSerPheLysSerIly----- 90
 QY 654 AAAACCTGAAGAGATGCTTTTGGACATTTCAAGCATCTGATGAAGAGTTCCTTAA 713
 Db 91 --MetLeuGlnIleuLysLeuIleAspThrPheLeuAlaThrAspValGluLeuLys 109
 QY 714 CAAGCTTCACCGAAGAGCTCCGTGAAGAGTGCACCTGACCGACGTGTGCTGCT 773
 Db 110 AspGluLysLeuAspAsp-----HisSerGlyCysThrAlaThrValIleLeuVal 127
 QY 774 -----GTACACAACTCTTATATTCAGCACTCCGAGATGATGAGGACATCTTGCT 827
 Db 128 SerGlnLeuLysLysLeuLeuIleCysAlaAsnSerGlyAspSerThrGlyValLeu 146
 QY 828 CGTTATATAGAGAGAGTCAAAAACATGACCTTAAGCTTCAGAAAGCATTAATCA 887
 Db 147 -----SerThrGlyLysAsnSerLysAlaMetSerPheAspHisLysPro 161
 QY 888 ACTCATATGAAGAGCGATGAGTACAGAAAGCTGAGAAACATCAGGAGTGGCGCT 947
 Db 162 ThrLeuLysSerIleLysSerThrGlyLeuAlaAlaAspGlyPheValGluMetAspArg 181
 QY 948 GTTTGGGCTGTGATGAGGTTCACGCTCCATTGGGGAGCGGACATCAAG----- 998
 Db 182 ValAsnGlyAsnLeuAlaLeuSerThrGlyAlaIleGlyAspPheGluPheLysSerAsnThr 201
 QY 999 CGTGGCGGT-----GTCACTCTGTGCCCCGACATCAGACGCTGCCAGCTG 1043
 Db 202 LysLeuGlyProHisGluGlnValAlaThrCysValProAspIleIleCysHisAsnLeu 221
 QY 1044 ACC---CCCAATGACAGATGCTATTTTGGCTGATGGGTGCTTCAAGGCTTTTAC 1100
 Db 222 AsnTyrAspGluAspGluPheValIleLeuAlaCysAspGlyIleTyrAspCysLeuThr 241
 QY 1101 CCAGAAAGCCGCTGACATTCATCTTCCTGCTGACAGATGAAGAATCCAGACCCGG 1160
 Db 242 SerGlnIleCysValAspLeuVal-----His 250
 QY 1161 GAAGGAAATCCCGACCCGACCCGCTGACAGACCTTCACACGCTGGCCACAC--- 1217
 Db 251 TyrIleLysSerIleGlnLysMetThrLeuSerAspIleSerSerThrIleValAspAl 270
 QY 1218 -----AAGCGGTGACGAGCGGGCTCG-----GCCGACAACTCATCTGTATGCTG 1262
 Db 271 CysCysSerProThrThrGlnGlySerGlyIleGlyCysAspAsnMetSerIleSerIle 290
 QY 1263 GTGGCGATA 1271
 Db 291 ValAlaLeu 293

RESULT 24
 PTC4_ARATH
 ID PTC4_ARATH STANDARD; PRT; 399 AA.
 AC P49598;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C (EC 3.1.3.16) (PTC2).
 GN AT1G11410 OR P24K9.8.
 OS Arabidopsis thaliana (Mouse-ear cress). Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=95116318; PubMed=7816619;
 RA Kurotori T., Yamamoto M.;
 RT "Cloning of cDNAs from Arabidopsis thaliana that encode putative
 protein phosphatase 2C and a human Drl-1-like protein by transformation
 of a fission yeast mutant.";

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RP SEQUENCE FROM N.A.
 Leung-Hagestedt J. C., Mahendra A., Naruszewicz I., Hamigan G.E.,
 RT "Modulation of integrin signal transduction by ILKAP, a protein
 RT phosphatase 2C associating with the integrin-linked kinase, ILK1.";
 RL EMBL J. 0:0-0(2001).

RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UTERUS;
 RA Strausberg R.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AL136850, CAB66784.1; -
 DR EMBL, AY024365, AAK07736.1; -
 DR EMBL, BC006576, AAH06576.1; -
 DR HSSP, P35813, 1A6Q.
 DR InterPro, IPR000222, PP2C.
 DR InterPro, IPR001932, PP2C-like.
 DR Pfam, PF00481, PP2C, 1.
 DR SMART, SM00332, PP2C, 1.
 DR SMART, SM00331, PP2C_SIG, 1.
 DR PROSITE, PS01032, PP2C, 1.
 KW Hypothetical protein; Kinase.
 SQ SEQUENCE 392 AA; 42906 MW; AF6AC98508CBEA3 CRC64;

Alignment Scores:
 Pred. No.: 1,28e-161 Length: 392
 Score: 2018.00 Matches: 392
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 78.83% Indels: 0
 DB: Gaps: 0

US-09-935-124a-1 (1-1422) x Q9H0C8 (1-392)

QY 102 ATGACCTCTTGGGGGACCTGGCGGAGCCGAGCGCTGGCGGCGCGCTGGCGGGAAA 161
 DB 1 MetAspLeuPheGlyAspLeuProGluProGluArgSerProAlaAlaGlyLys 20
 QY 162 GAAGCTCAGAAAGAGACCCCTGCTTTGATGACCTCCCTCCGCGCAGCAGTACTGACTCA 221
 DB 21 GluAlaGlnLysGlyProLeuLeuPheAspLeuProAlaSerSerThrAspSer 40
 QY 222 GATTCAGGGGGACCTTGGCTTTTGTATGATCTCCACCCGCTAGCGGCGCATTCAGGT 281
 DB 41 GlySerGlyGlyProLeuLeuPheAspLeuProAlaSerSerGlyAspSerGly 60
 QY 282 TCTCTGGCCATCAATATCCGATGCTGAAGCTGAAGCGAAAGGAGAAAGAGAAA 341
 DB 61 SerLeuAlaThrSerIleSerGlnMetValLysThrGluLysGlyAlaLysArgLys 80
 QY 342 ACCTCCGAGAGAAAGAAATGCGCAGTGAAGACTGTGGAAAAGAAATTTGTAAAGCC 401
 DB 81 ThrSerGluGluGluLysAsnGlySerGluGluLeuValGluLysLysValCysLysAla 100
 QY 402 TCTTCGGTATCTTGGCTGGAAGGCTATGTGGCTGAGCGGAAAGGTGAGAGAGAG 461
 DB 101 SerSerValIlePheGlyLeuLysGlyTyrValAlaGluArgLysGlyGluArgGlu 120
 QY 462 ATGACGAGATCCACGCTCATCCGAGATCAACGAGAGGTAGGCCCCCATGCTCC 521
 DB 121 MetGlnAspAlaIleValIleLeuAsnAspIleThrGluLysCysArgProPheSer 140
 QY 522 CTCATTAAGTGGGTTTCATATTTTGTGCTTTTGTATGATGAGATGAGAGAAATTCAGCCTCA 581
 DB 141 LeuIleThrArgValSerTyrPheAlaValPheAspGlyIleGlyIleAlaGlnAsp 160
 QY 582 AAATTTGCTGCACAGATTTGATCAAACTTAATCAGAAAATTTCTTAAGAGATGTA 641
 DB 161 LysPheAlaIleAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
 QY 642 ATAGAGTGAAGAAAACCGTGAAGAGATGCTTTTGAACATTTCAAGCATTAATGATGAA 701
 DB 181 IleSerValGluLysThrValLysArgCysLeuLeuAspThrPheLysHisIleThrAspGlu 200

QY 702 GAGTTCCTTAAACAAAGCTTCCAGCCAGAAAGCCTGCTGGAAAGATGGTCCATGCCACG 761
 DB 201 GluPheLeuLysGlnAlaSerSerGlnLysProAlaIleLysAspGlySerThrIleThr 220
 QY 762 TGTGTCTGGCGTGTGACAACTTCTTATATTTGCAACCTCGGAGATGTGCGGCAATC 821
 DB 221 CysValLeuAlaValAspAsnIleLeuTyrIleAlaAsnGlyLysSerArgAlaIle 240
 QY 822 TTGTGCTGTATATAGAGAGAGATCAAAAACATGACGCTTAAGCTCAGCAAGAGCAT 881
 DB 241 LeuCysArgTyrAsnGluLysSerGlnLysHisAlaAlaLeuSerLeuSerLysGlnHis 260
 QY 882 AATCCAACTCAGATGAGAGCGGATGAGATACAGAAAGCTGAGAGAAAGCTCAGGGAT 941
 DB 261 AsnProThrGlnTyrGluGluLysArgLysGlnLysAlaGlyLysValArgAsp 280
 QY 942 GGGCGGTGTTTGGCGGTGTAGAGTGCACGCTCATTTGGGAGCGGCGAGTCAAGACGC 1001
 DB 281 GlyArgValLeuGlyValLeuGluValSerArgSerIleGlyAspGlyGlnTyrLysArg 300
 QY 1002 TCGGCTGACCTCTGTGCGCCGACATCAGACGCTGACGCTGACCCCAATGACAGTTTC 1061
 DB 301 CysGlyValThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
 QY 1062 ATTTGTGGCTGTGATGAGGCTCTTCAAGTCTTTACCCCAAGAAAGCCGTGAACCTTC 1121
 DB 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheThrProGluGluAlaValAsnPhe 340
 QY 1122 ATCTTGCTCTGTCTGAGAGATGAAAGATCCAGACCCGGGAGGAGATCCGACCCGAC 1181
 DB 341 IleLeuSerCysLeuGluLysPheGluLysIleGlnThrArgGluLysSerAlaAsp 360
 QY 1182 GCCCGCTAAGAGCAGCCTCGCAACAGCTGCGCAACAAAGCGGTGACGCGGCTCGCGC 1241
 DB 361 AlaArgTyrGluAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgLysSerAla 380
 QY 1242 GACAACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1277
 DB 381 AspAsnValThrValMetValValArgIleGlyHis 392

RESULT 2

Q8ROF6 PRELIMINARY PRT; 392 AA.
 ID Q8ROF6;
 AC Q8ROF6;
 DT 01-JUN-2002 (TREMblrel. 21, Created)
 DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
 DE Similar to protein phosphatase 2C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN NCBI_TaxID=10090;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Strausberg R.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC026953, AAH26953.1; -
 SQ SEQUENCE 392 AA; 42774 MW; 8DE1F77DDAC9B7176 CRC64;

Alignment Scores:
 Pred. No.: 1,29e-154 Length: 392
 Score: 1935.00 Matches: 373
 Percent Similarity: 97.70% Conservative: 10
 Best Local Similarity: 95.15% Mismatches: 9
 Query Match: 75.59% Indels: 0
 DB: Gaps: 0

US-09-935-124a-1 (1-1422) x Q8ROF6 (1-392)

QY 102 ATGACCTCTTGGGGGACCTGGCGGAGCCGAGCGCTGGCGGCGCGCTGGCGGGAAA 161
 DB 1 MetAspLeuPheGlyAspLeuProGluProGluArgAlaProArgProSerAlaGlyLys 20

[illegible]

Oy	1242	GACAGCCTGACTGATGTGGTGGATTGGGCAC	1277
Dd	381	AspaenvalThrValMetcaValArgIleGlyHis	392
 RESULT 3			
ID	Q9Z1Z6	PRELIMINARY:	PRT; 392 AA.
MC	Q9Z1Z6;		
DT	01-MAY-1999	(TrEMBLrel. 10, Created)	
DT	01-MAY-1999	(TrEMBLrel. 10, Last sequence update)	
DT	01-MAY-2002	(TrEMBLrel. 20, Last annotation update)	
DE	Protein phosphatase 2C.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=9074314; PubMed=9857069;		
RA	Tong Y., Quirion R., Shen S.H.;		
RT	"Cloning and characterization of a novel mammalian PP2C isozyme.";		
RL	J. Biol. Chem. 273(35282-35290(1998).		
DR	EMBL; AF095927; AAC97497.1; -.		
DR	HSSP; P35813; IAGQ.		
DR	InterPro; IPRO00222; PP2C.		
DR	InterPro; IPRO01932; PP2C-like.		
DR	Pfam; PF00481; PP2C; 1.		
DR	SMART; SM00332; PPCc; 1.		
DR	SMART; SM00331; PPCc StG; 1.		
DR	PROSITE; PS01037; PP2C; 1.		
SQ	SEQUENCE 392 AA; 42744 MW; 1468FDB0BA60D915 CRC64;		
 Alignment Scores:			
Score:	No.: 2,816-154	Length:	392
Percent Similarity:	1931.00	Matches:	373
Best Local Similarity:	96.94%	Conservative:	7
Query Match:	75.13%	Mismatches:	12
DB:	I1	Indels:	0
		Gaps:	0
 US-09-935-124A-1 (1-1422) x Q9Z1Z6 (1-392)			
Oy	102	ATGAGACTCTTCGGGGAACTCGCCGAGCCGGAAGCGCTGCCGCCGCCGCTCCGGGAAA	161
Dd	1	MeIAapLeuPheglYasPLeuPProgluIPProgluIRProfoIRProseIRlaIdgLyIs	20
Oy	162	GAAGTCAGAAAGAGACCCTCGCTCTTTGATGACCTCCCTCGGCACAGTACTGATCA	221
Dd	21	GIuaIagIngluglYroValLeuPheGlAaPLeuProporIRserSerThrIaPser	40
Oy	222	GGATCAGGGGGACCTTTCGCTTTTGATGATCTCCACCGCATGACATGCGCATGAGT	281
Dd	41	GlyserIGlyglYProleuLeuPhehPegolYLeuPProfoIRlaIdyserIGlyamserIdg	60
Oy	282	TCTCTTGGCAATCAATATTCGCCAGTGTAAAGATGAAAGGAAAGAGCAAAAGAAAA	341
Dd	61	SeIeuLeuIathIRserIdgYserIdnValValYaaIngIluglYrgolYAlaYarIgys	80
Oy	342	AACCTCCGAGAAGAAAGAAAGCAGCGAAGCTTTCGAAAAGAAAGTTGTAAGCC	401
Dd	81	AIaP-ProgluIngluYaaMendYelYelIngluLeuValGIuYbuYalCPuYsaIa	100
Oy	402	TCTTCGATGATCTTTCGTTGAAAGGCTATATGCGCTAGACCGAAGGGTGAAGAGAG	461
Dd	101	SeISerVaIIIEPegIyeuYseIYTYVaIIaIaGluaYrIVSglYluIrIagluIn	120
Oy	462	ATGCAGAGTCCACGTCATCTCTGAACGACATCACCGAGAGTGTAGGCCCCCATCTGCC	521
Dd	121	MeGIaPaPalahIaVallIEleaMaSPRIethGIngluCYaaIPProfoIRser	140
Oy	522	CTCATTAATCGGGTTTCATATTTTCGTTTTTGATGACANYGAGGAATTCGACCTCA	581
Dd	141	IeuIIeIRhaYgaIaSerYrheIaIaIaPheASpGylNhgIyglYIeIRgaIaSer	160

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QY 582 AAATTGTCGACAGAAATTTGATCAAACTTAATCAGAAATTTCTTAAGGAGATGTA 641
    |||||
Db 161 LysPheAlaIaIeGlnIleuNhiSegInAenIleIaRgLySerProIySglYAspVal 180
QY 642 ATCAGCTGTAGAGAAAACCGTGAAGAGATGCTTTTGACACTTTCAAGCTACTGATGAA 701
    |||||
Db 181 ILeSerValGlnLysThrValIySAsrGySleuLeuAspThrPheYshIstThaRspGln 200
QY 702 GAGTTCCTTAACAGACTTCACAGAGCCGCTGGAAGAGATGAGTTCACCTGACAG 761
    |||||
Db 201 GluPheLeuLysGlnIaSerSerGlnLysProAlaItrPlyAspGlySerThraIaThr 220
QY 762 TGTGTTCTGAGCTGTAGACAACTTTCTTAATTTATTTGCAACCTCGAGATAGTGGGCAATC 821
    |||||
Db 221 CysValIleuAlaValaIePheNhiIeLeuYrIleAlaAsnLeuLysPheSerAlaIle 240
QY 822 TTGTGCTGTTATATAGAGAGAGTCAAAAACATGACGCTTAAGCTCAGCAAAAGCAT 881
    |||||
Db 241 LeuCyAsrGlyrAsnGlnLysSerGlnLysHsAlaAlaIeSerIeSerLysGlnHs 260
QY 882 AATCAACTCAGATATAGAGAGCGATGAGGATACAGAGGCTGAGAGAAACGTGAGGAT 941
    |||||
Db 261 AsnProThrGlnYrGlnLysGlnMetArgIleGlnLysAlaIleYglYAsnValaItrAsp 280
QY 942 GGGCGTGTGTTGGGCGTGTAGAGTGTACAGCTCCATTTGGGAGCGGAGTACAAAGCC 1001
    |||||
Db 281 GYArGValIeugLylValIeugLysValSerArgSerIleGlyAspGlyGlnYrLysArg 300
QY 1002 TGGGCTGACCTCTGTGCGGACATCAGAGCTGCCAGCTGACCCCAATGACAGCTTC 1061
    |||||
Db 301 CySgLYValIthSerValIProAspIleArGArgCySgIleuThrProAsnAspArgPhe 320
QY 1062 ATTTGTGTGGCCGTGATGGGCTTCAAGGCTTTATACCCAGAAAGCCGGAAGCTTC 1121
    |||||
Db 321 IleLeuLeuAlaIeCyAspGlyLeuPheLysValPheThrProGlnLysAlaValaIAspPhe 340
QY 1122 ATCTGTCTGTCTCGAGATGAAAAGATCCAGACCCGGGAGAGGAGTCCGACGCGAC 1181
    |||||
Db 341 IleLeuSerCysLeuGlnLysArgGlyIleGlnIthArgGlnLysProAlaValaIAsp 360
QY 1182 GCGCGCTGACGAGAGCCCTGCAACAGAGCTGGCCCAACAGAGCGGCTGACGCGGCTCGGCC 1241
    |||||
Db 361 AlArGlyrGlnLysAlaIeCyAsnArGLeuAlaAsnLysAlaValaIleGlnArgIle 380
QY 1242 GACAAGCTGATGATGGTGTGGGATGAGGAC 1277
    |||||
Db 381 AspAsnValIthValaIeValaIAsrIleGlyHs 392

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RESULT 4

```

Q9DC99 PRELIMINARY: PRT: 272 AA.
AC Q9DC99:
DT 01-0UN-2001 (TrEMBLrel. 17, Created)
DT 01-0UN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 0710007A1ARIK protein.
GN 0710007A1ARIK
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=BRAIN;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

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RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guerinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombers P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK003007; BAB22508.1; -.
DR HSSP; P35813; 1A6Q.
DR MGI; MGI:1914694; 0710007A1ARIK.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 272 AA; 30279 MW; 485F2959D91BA63D CRC64;

Alignment Scores:
Pred. No.: 2,37e-108 Length: 272
Score: 1386.00 Matches: 266
Percent Similarity: 98.90% Conservative: 3
Best Local Similarity: 97.79% Mismatches: 3
Query Match: 54.14% Indels: 0
DB: Gaps: 0

US-09-935-124A-1 (1-1422) x Q9DC99 (1-272)
QY 462 ATGACGAGATGCCAGCTATCTGTAAGCATCACCAGAGATGAGGCCCATCTGTC 521
    |||||
Db 1 MetGlnAspAlaIeValIleLeuAsnAspIleTrGlnGlnCyAsnProProSer 20
QY 522 CTCATTACTCGGGGTTTCATATTTCTGTTTGTATGAGCATGAGGAAATGAGCTCA 581
    |||||
Db 21 LeuIleThrArgValSerTrPheAlaValIlePheAspGlyHsGlyYIleArgAlaSer 40
QY 582 AAATTGTCGACAGAAATTTGATCAAACTTAATCAGAAATTTCTTAAGGAGATGTA 641
    |||||
Db 41 LysPheAlaIaIeGlnIleuNhiSegInAenIleIaRgLySerProIySglYAspVal 60
QY 642 ATCAGCTGTAGAGAAAACCGTGAAGAGATGCTTTTGACACTTTCAAGCTACTGATGAA 701
    |||||
Db 61 ILeSerValGlnLysThrValIySAsrGySleuLeuAspThrPheYshIstThaRspGln 80
QY 702 GAGTTCCTTAACAGACTTCACAGAGCCGCTGGAAGAGATGAGTTCACCTGACAG 761
    |||||
Db 81 GluPheLeuLysGlnIaSerSerGlnLysProAlaItrPlyAspGlySerThraIaThr 100
QY 762 TGTGTTCTGAGCTGTAGACAACTTTCTTAATTTATTTGCAACCTCGAGATAGTGGGCAATC 821
    |||||
Db 101 CysValIleuAlaValaIePheNhiIeLeuYrIleAlaAsnLeuLysPheSerAlaIle 120
QY 822 TTGTGCTGTTATATAGAGAGAGTCAAAAACATGACGCTTAAGCTCAGCAAAAGCAT 881
    |||||
Db 121 LeuCyAsrGlyrAsnGlnLysSerGlnLysHsAlaAlaIeSerIeSerLysGlnHs 140
QY 882 AATCAACTCAGATATAGAGAGCGATGAGGATACAGAGGCTGAGAGAAACGTGAGGAT 941
    |||||
Db 141 AsnProThrGlnYrGlnLysGlnMetArgIleGlnLysAlaIleYglYAsnValaItrAsp 160
QY 942 GGGCGTGTGTTGGGCGTGTAGAGTGTACAGCTCCATTTGGGAGCGGAGTACAAAGCC 1001
    |||||
Db 161 GYArGValIeugLylValIeugLysValSerArgSerIleGlyAspGlyGlnYrLysArg 180
QY 1002 TGGGCTGACCTCTGTGCGGACATCAGAGCTGCCAGCTGACCCCAATGACAGCTTC 1061
    |||||
Db 181 CySgLYValIthSerValIProAspIleArGArgCySgIleuThrProAsnAspArgPhe 200

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QY 1062 ATTTGTGCTGTGATGGGCTCTTCAAGGCTCTTTACCCCAAGAAAGCCGTGAATTC 1121
DB 201 TTTCTCTTAAACAAAGCTTCCAGCAAGAAAGCTGCTGGAAGAATGGCTCCATGCGCAG 761
QY 1122 ATCTTGCTCTGTCTGAGATGAAAGATCCAGACCCGGGAAAGGAAAGTCCGACGCCAG 1181
DB 221 TTTCTCTTAAACAAAGCTTCCAGCAAGAAAGCTGCTGGAAGAATGGCTCCATGCGCAG 761
QY 1182 GCCCGCTACGAGAGCCCTGCAACAGGCTGGCCCAAGAGCGGTGACGCGGGCTCGGCC 1241
DB 241 AATAGTGTGTGTAATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATG 260
QY 1242 GACAAGCTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1277
DB 261 AAAAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 272

RESULT 5
Q9CS46 PRELIMINARY; PRT; 212 AA.
AC Q9CS46;
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 0710007A14R1K.
GN 0710007A14R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRIO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shigaawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saio T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saio R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Knehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki K., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Fujino M., Kono H., Balderelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gietzung S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni B., Mashima Y., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohenki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL/ AK019158; BAB31574.1; -.
DR HSSP/ P35813; IAG6.
DR MGD/ MGI:1914694; 0710007A14R1K.
DR InterPro/ IPR001932; P2C-like.
DR Pfam/ PF00481; P2C; 1.
DR SMART/ SM00332; P2C; 1.
FT NON TER 1
SQ SEQUENCE 212 AA; 23615 MW; 133286D628B540D7 CRC64;

Alignment Scores:
Pred. No.: 2,11e-82 Length: 212
Score: 1078.00 Matches: 208
Percent Similarity: 99.06% Conservative: 2
Best Local Similarity: 98.11% Mismatches: 2
Query Match: 42.11% Indels: 0
Gaps: 0

US-09-935-124a-1 (1-1422) x Q9CS46 (1-212)

QY 642 ATCAGGTAGAGAAACCGTAGAGAGATGCTTTGACACTTTCAAGCATCTGATGAA 701
DB 1 TTTCTCTTAAACAAAGCTTCCAGCAAGAAAGCTGCTGGAAGAATGGCTCCATGCGCAG 761
QY 702 GACTTCCTTAAACAAAGCTTCCAGCAAGAAAGCTGCTGGAAGAATGGCTCCATGCGCAG 761
DB 21 GTPheLeuValGlnValAspSerGlnValProIleTyrValAspGlySerThrIleThr 40
QY 762 TGTGTCTGTATATGAGAGAGTCAAAACATGACGCTTAACTCAGCAAGAGCT 821
DB 41 CysValLeuValAspSerIleLeuTyrIleIleAsnLeuGlyAspSerAlaIle 60
QY 822 TGTGTCTGTATATGAGAGAGTCAAAACATGACGCTTAACTCAGCAAGAGCT 881
DB 61 LeuValGlnValAspSerIleLeuTyrIleIleAsnLeuGlyAspSerAlaIle 80
QY 882 AATCAACTCACTATGAGAGAGTCAAAACATGACGCTTAACTCAGCAAGAGCT 941
DB 81 AsnProThrGlnTyrGlnGluArgMetArgIleGlnValAspGlyValAsnValArgAsp 100
QY 942 GGGCGTGTGTGGGCGTGTGAGAGTGTCAAGCTCATTGGGAGACGGCAGTCAAGCGC 1001
DB 101 G1ArgValIleGlnValIleGlnValIleValSerArgSerIleG1ArgValIleTyrValArg 120
QY 1002 TGGGAGTCACTCTGTGCGCCAGCATGACAGCGTGCAGCTGACCCCAATGACAGGTT 1061
DB 121 CysGlyValIleThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 140
QY 1062 ATTTGTGCTGTGATGGGCTCTTCAAGGCTCTTTACCCCAAGAAAGCCGTGAATTC 1121
DB 141 TTTCTCTTAAACAAAGCTTCCAGCAAGAAAGCTGCTGGAAGAATGGCTCCATGCGCAG 1181
QY 1122 ATCTTGCTCTGTCTGAGATGAAAGATCCAGACCCGGGAAAGGAAAGTCCGACGCCAG 1181
DB 161 TTTCTCTTAAACAAAGCTTCCAGCAAGAAAGCTGCTGGAAGAATGGCTCCATGCGCAG 1181
QY 1182 GCCCGCTACGAGAGCCCTGCAACAGGCTGGCCCAAGAGCGGTGACGCGGGCTCGGCC 1241
DB 181 AATAGTGTGTGTAATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATGAAAGATG 260
QY 1242 GACAAGCTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1277
DB 201 AAAAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 272

RESULT 6
Q920T2 PRELIMINARY; PRT; 167 AA.
AC Q920T2;
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 18.8 kDa protein (Fragment).
GN 0710007A14R1K.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG;
RA Stochard P.W., Pilgrim D.;
RT "Isolation of P2C sequences using degenerate-oligo PCR.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBO databases.
DR EMBL/ AF117831; AAD17234.1; -.
DR HSSP/ P35813; IAG6.
DR MGD/ MGI:1914694; 0710007A14R1K.
DR InterPro/ IPR001932; P2C-like.
DR Pfam/ PF00481; P2C; 1.
DR SMART/ SM00332; P2C; 1.
DR Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 167 AA; 18795 MW; 3A4FC2EFB09D95B CRC64;

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Alignment Scores:

Pred. No.:	1,04e-63	Length:	167
Score:	856.00	Matches:	165
Percent Similarity:	99.40%	Conservative:	1
Best Local Similarity:	98.80%	Mismatches:	1
Query Match:	33.44%	Indels:	0
DB:	11	Gaps:	0

US-09-935-124A-1 (1-1422) x Q9ZMT1 (1-167)

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QY 570 ATTGCAAGCTCAAAATTTGCTGACAGAAATTTGATCAAAATTTATTCGAAATTTCTT 629
Db 1 TLeaTgAlaSerLySeuAlaAlaGlnAenLeuHLeGlnAenLeuIleArgLySephro 20
QY 630 AAGGAGATGATATCATGCTAGAGAAAACGGTGAAGAGATGCTTTTGACCTTTCAAG 689
Db 21 LysGlyAspRileIleSerValGluLysTrnValLysArgCysLeuAenAspTrnPhelys 40
QY 690 CATACTGATGAAGAGTTCTTAAACAAGCTTCCAGCCAGAGAGCTGCGAAGATGGG 749
Db 41 HleTrnAspGluGluPhelLeuLysGlnAlaSerSerGlnLysProAlaTrpLysAspGly 60
QY 750 TCCACTGCCACGTGTCTGCTGCTGACACACATTTCTTATTTATTTCCCAACTCGAGAT 809
Db 61 SerTrnAlaThrCysValLeuAlaValaAspAenIleLeuTrpIleAlaAenLeuGlyAsp 80
QY 810 ACTCGGGCAATCTGTGTGCTTATATATGAGAGAGTCAAAAACATGACGCTTAAAGCTC 869
Db 81 SerTrnAlaIleLeuCysArgTrpAenGluGluSerGlnLysHleAlaAenSerLeu 100
QY 870 AGCAAAAGACATATTCACATCAGTATGAAGAAGCGGATGAGATACAGAAGCTGAGAGA 929
Db 101 SerLySGluHleAenProThrGlnTrpGlnLysArgMetArgIleGlnLysAlaGlyGly 120
QY 930 AACGTCAAGGATGGGCGTGTGTTGGCGCTGCTGACAGTGTCAAGCTTGGGACGGG 989
Db 121 AenValaArgAspGlyArgValLeuGlyValLeuGlnValaSerArgSerIleGlyAspGly 140
QY 990 CAGTCAAGCGCTGGCGGTGACCTGTGCGCCGACATACAGCGCTGACGAGTCAAGCCCC 1049
Db 141 GlnTrpLysArgCysGlyValTrnSerValProAspRileArgLysGlnLeuTrnPro 160
QY 1050 AATGACAGGTTTCATTTGTTG 1070
Db 161 AenAspArgPheIleLeuLeu 167

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RESULT 7

Q9ZMT1 PRELIMINARY; PRT; 341 AA.

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AC Q9ZMT1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE T10F20.4 Protein.
GN T10F20.4.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucotyle II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sakano H., Liu S.X., Egu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
RA Yu G., Chan A., Chung M., Goldemich A., Liu A., Smith A., Vaynsberg M.,
RA Alefai H., Brooks S., Buehler B., Chao Q., Conn L., Conway A.B.,
RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
RA Federpriel N.A., Theologis A.;
RT "The sequence of BAC T10F20 from Arabidopsis thaliana chromosome 1.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL; AC034107; AAF97840.1; -.

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DR HSBP; P35813; 1A6Q.
DR InterPro; IPR001932; PP2C-1like.
DR Pfam; PF00481; PP2C_1.
DR SMART; SM00332; PP2C_1.
DR SMART; SM00331; PP2C_SIG; 1.
SQ SEQUENCE 341 AA; 37367 MW; 6873C0CB82310195 CRC64;

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Alignment Scores:

Pred. No.:	5.75e-32	Length:	341
Score:	481.00	Matches:	119
Percent Similarity:	55.72%	Conservative:	66
Best Local Similarity:	35.84%	Mismatches:	107
Query Match:	18.79%	Indels:	40
DB:	10	Gaps:	11

US-09-935-124A-1 (1-1422) x Q9ZMT1 (1-341)

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QY 333 AAGAGAAAACCTCCGAGAGAGAGAAATGCGACTGAAGCTTGTG----- 380
Db 24 LysAlaLysLysSerGluGluValSerGlyGlyGluAlaValAlaAlaValGlyAen 43
QY 381 ---GAAAGAAAGTTGTAAAGCCCTTCGGATC-----TTTGCTG 422
Db 44 ArgGluAlaGluGluAspLysProSerPheValSerGluGluLysLysGluPhelVal 63
QY 423 AAGGCTATGTGCTGACGCGAAGGCTGAGAGGAGAGATGCAGATGCCACGCTCATC 482
Db 64 GluAlaAspValAlaGluAspLysGlyAlaArgHleTrnMetGluAspValTrpValVal 83
QY 483 CTGAAGCAATCACCAGAGAGTGAAGCCCCCATGCTCCCTCATTAAGCTGGGTTTCAT 542
Db 84 LeuProAspAlaSerLeuAspPhe-----ProGlyTrnLeu-----ArgCysAlaHis 99
QY 543 TTTGCTGTTTGAATGACATGAGAGAAATGAGGCTCAAAATTTGCTGACAGAAATTTG 602
Db 100 PheAlaIleTrpAspGlyHisGlyGlyArgLeuAlaAlaGluPheAlaLysLysHleu 119
QY 603 CATCAAACTTATATGAGAAAATTTCTTAAAGAGATGTATATCAGTGAAGAAACCGTG 662
Db 120 HisLeuAenValLeuSerAlaGlyLeuProArgGluLeuLeuAspVal---LysValAla 138
QY 663 AAGAGATCCCTTTTGACACATTTCAAGCATCTGATGAAGATCTTAAACAAGCTTCC 722
Db 139 LysLysAlaIleLeuGluGlyPheArgLysTrnArgGluLeuLeuGlnLysSerVal 158
QY 723 AGCCAGAAAGCTCGTGAAGAAGTGGTCCATCGTCCAGTGTCTGAGTGTATACAC 782
Db 159 Ser-----GlyGlyTrpGlnAspGlyAlaTrnAlaValCysValTrpIleLeuAspGln 176
QY 783 ATTCTTATATGCGCAACCTGAGATAGTGGGCAATCTTGTCGT----- 830
Db 177 LysValAlaPheValAlaAenIleGlyAspAlaLysValAlaValaLysSerSerThrTrn 196
QY 831 -----TATATGAGAGAGTCAAAAACATGCAAGCTTAAAGCTTCAAGAA 875
Db 197 AenGluLeuGlyAenHisThrGluAlaGlyAenProLeuLysAlaIleValLeuThrArg 216
QY 876 GAGCATATTCACATCAGTATGAAGAAGGAGTGAAGATACAGAAAGCTGAGAGAAAGCTC 935
Db 217 GluHisLysValaIleTrpProGlnTrnLysSerArgIleGlnLysSerGlyGlyValIle 236
QY 936 ---AAGGATGGGCGTGTGCTGCTGACGCTGATGAGTGCACCTCATTTGGGAGCGGAG 992
Db 237 SerSerAenGlyArgLeuGlnGlyArgLeuGluValaSerArgAlaPheGlyAspArgHis 256
QY 993 TACAAGCGCTGGGCTGACCTTGTGCGCCAGATCAGACGCTGCGACGTGACCCCAAT 1052
Db 257 PheLysLysPheGlyValaSerAlaThrProAspRileHisAlaPheGluLeuThrLysArg 276
QY 1053 GACAGTTCATTTTGTGCTGTGATGGGCTCTTCAAGAGTCTTTAACCACAGAAAGCC 1112
Db 277 GluAenPheMetIleLeuGlyCysAspGlyLeuTrpGluValPheGlyProSerAspAla 296

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QY 1113 GTGAACTTCATCTTCTCTCTCTCTCGAGATGAAAAAGATCCAGACCCCGGGAAGGAATGCC 1172
DB 297 ValGlyPheValGlnIleuLeu-----LysGlnGly----- 307
QY 1173 GCAGCCGACGCGCCGTCAGAAAGAGCTTCAGACGGCTGGCCAAAGCGCGTG---CAG 1229
DB 308 -----LeuHleValSerThValSerArgGlyLeuValLysGlnLalaValLysGln 324
QY 1230 CGGGGCTCGGCGGACCAAGTCATCTGATGGTGCTG 1265
DB 325 ArgArgCysLysAspAsnCysThrAlaIleValIle 336
RESULT 8
O944K0
ID O944K0 PRELIMINARY; PRT; 351 AA.
AC O944K0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2002 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE At1g18030/T10F20.3
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Euphorbia II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxId=3702;
(1)
RA SEQUENCE FROM N.A.
RA Chew R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carrinci P., Dale J.M., Goldsmith A.D., Hayaishiaki Y.,
RA Ihida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.T., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RA "Arabidopsis cDNA clones.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF428352; AAL16282.1; -.
DR InterPro; IPR001932; P2C-like.
DR Pfam; PF00481; P2C; 1.
SQ SEQUENCE 351 AA; 38514 MW; AFE22480E003229 CRC64;

Alignment Scores:
Pred. No.: 7,05e-32 Length: 351
Score: 480.00 Matches: 119
Percent Similarity: 55.72% Conservative: 66
Best Local Similarity: 35.94% Mismatches: 107
Query Match: 18.75% Indels: 40
DB: 10 Gaps: 11

US-09-935-124A-1 (1-1422) x O944K0 (1-351)
QY 333 AAGAGAAAACCTCCGAGAGAGAGAAATGCGAGTGAAGCTTGTC----- 380
DB 34 LysAlaLysLysSerGlnGlnLysSerGlnLysGlnLysAlaLysAlaLysAlaLysAsn 53
QY 381 ---GAAAAAGAAAGTTGTAAAGCTCTTCGGTGATC-----TTTGGTCTG 422
DB 54 ArgGlnValGlnGlnLysPheSerPheValSerGlnLysLysGlnLysLeuVal 73
QY 423 AAGGGCTATGTGCTGAGCGGAAAGGAGTGAAGAGAGATGAGAGATCCCAAGCTCATC 482
DB 74 GluAlaSerValAlaGlnLysPheLysGlyAlaArgHisThrIleGlnLysValTyrValTyr 93
QY 483 CTGAACGACATCACCGGAGGTGTAGCGCCCATCGCTCATCTACTCGGTTTCATAT 542
DB 94 LeuProAspAlaSerLeuAspPhe-----ProGlyThrLeu-----ArgCysAlaHis 109
QY 543 TTTGCTGTTTTGATGAGCATGAGAGAAATTCGAGCTTCAGAAATTTGTCGACAGAAATTTG 602
DB 110 PheAlaIleTyrTrpAspGlyHisGlyGlyArgLeuAlaLysGlnLysAlaLysHisLeu 129
QY 603 CATCAAACTTAATCAGAAAAATTTCTTAAGAGAGATGTATCATGCTGAGAAAAACGTG 662

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DB 130 HisLeuAsnValLeuSerAlaGlyLeuProArgGlnIleLeuLeuAspVal---LysValAla 148
QY 663 AAGAGATGCGCTTTGTGACATTTTCAAGCATATCATGATGAAGAGTTCTTAAACAAGCTTC 722
DB 149 LysLysAlaIleIleGlnGlnGlyPheArgLysThrAspGlnLysLeuLeuGlnLysSerVal 168
QY 723 AGCCAGAACCTCGCTCGGAAGAAGAGGTGCATCGCCAGCGATGTTCTCGGCTGTGAACAAC 782
DB 169 Ser-----GlyGlyTyrGlnAspGlyAlaIleThrAlaValCysValTyrLysLeuAspGln 186
QY 783 ATTCTTATATTTGCCAACCTCGGATGATCGGGCAATTTGTGCTG----- 830
DB 187 LysValPheValAlaAsnIleGlyAspAlaLysValAlaValLeuAlaArgSerSerThrThr 206
QY 831 -----TATATGAGAGAGATCAAAAACATGCAAGCTTAAAGCTTCAGCAAA 875
DB 207 AsnGlnLeuGlnYAsnHisThrGlnAlaGlyAsnProLeuLysAlaIleValLeuThrArg 226
QY 876 GAGCATATTCCAACTCAGATATGAAGAAGCGGATGAGATACAGAAAGCTGAGAAAGCTC 935
DB 227 GlnHisLysAlaIleTyrProGlnLysArgSerArgIleGlnLysSerGlyGlyValIle 246
QY 936 ---AGGATGGGCGTGTGTTGGGCGTGTAGAGTGTCAAGTGTCCATGGGGAGCGGACG 992
DB 247 SerSerAsnGlnYArgLeuGlnGlyArgLeuGlnValSerArgAlaPheGlyAspArgHis 266
QY 993 TACAAGCGCGTGGGCTGACCTGTGCGCCGACATCAGACGCTGCAACCCCAAT 1052
DB 267 PheLysLysPheLysLysAlaSerAlaThrProAspIleHisAlaPheGlnLeuThrGlnArg 286
QY 1053 GACAGGTTCACTTTGTTGGCCCTGAGAGGCTCTTCAGAGTCTTAAACCCAGAAAGAGCC 1112
DB 287 GlnAsnPheIleGlnLeuGlnCysAspGlyLeuTyrGlnValPheGlnProSerAspAla 306
QY 1113 GTGAATTCATCTTCTCTCTCTCTCGAGATGAAAAAGATCCAGACCCCGGGAAGGAATGCC 1172
DB 307 ValGlyPheValGlnIleuLeu-----LysGlnGly----- 317
QY 1173 GCAGCCGACGCGCCGTCAGAAAGAGCTTCAGACGGCTGGCCAAAGCGCGTG---CAG 1229
DB 318 -----LeuHleValSerThValSerArgGlyLeuValLysGlnLalaValLysGln 334
QY 1230 CGGGGCTCGGCGGACCAAGTCATCTGATGGTGCTG 1265
DB 335 ArgArgCysLysAspAsnCysThrAlaIleValIle 346
RESULT 9
O62212
ID O62212 PRELIMINARY; PRT; 242 AA.
AC O62212;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE F33A8.6 protein.
GN F33A8.6
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Rhabditidae; Caenorhabditis.
OX NCBI_TaxId=6239;
(1)
RA SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copestey T., Cooper J., Fulton L.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

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Db 156 -----AlaIleAlaValSerArgPheIleProAlaGlnSerArgPhe 170
Qy 903 CGGATGAGATACAGAGGCTGGAGAAAGCTCAGG-----GATGGGCGTGTGG 953
Db 171 ArgGlnArgIleGluAspAlaGlyGlyPheValMetTrpAlaGlyThrTrpArgValGly 190
Qy 954 GGGGCTGTAAGGTGTCAAGCTCCATTGGGGAGCGGGAGTACAAAGCCCTGGGTGACC 1013
Db 191 GlyValLeuAlaValSerArgAlaPheGlyAspLysLeuLeuLysGlnIleTyr--ValVal 209
Qy 1014 TCTGTGCCCCGACATCAGACGCTGCAGTGAACCCCAATGACAGTTTCATTTGTGGCC 1073
Db 210 AlaAspProGluIleGlnGluGluValValAspSerSerLeuGluPheLeuAla 229
Qy 1074 TGTGATGGCTCTTCAAGCTCTTAACTCCAGAGAAGCGGTGAACCTTCATCTGTCTGT 1133
Db 230 SerAspGlyLeuTrpAspValValThrAsnGluGluAlaValThrMetVal----- 246
Qy 1134 CTCGAGAGTAAAGATCCAGACCCGGAGAGGAGATCGCGACGCCGCTACGAA 1193
Db 247 -----LysProIleGlnAspThr-----Glu 253
Qy 1194 GCAGCTCGCAAGAGCTGGCCCAAGAGCGGTGCGAGCGGCTGCGCCAGCAAGCTACT 1253
Db 254 GluAlaAlaLysLysLeuMetGlnGlnAlaTyrGlnArgGlySerAlaAspAsnIleThr 273
Qy 1254 GTGATGTGTGTGCGG 1268
Db 274 CysValValValArg 278

RESULT 11
Q8RXV3 PRELIMINARY; PRT; 311 AA.
AC Q8RXV3;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 33.2 kDa protein.
GN AT4G31750.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Cahini P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kaniya A., Karlin-Neumann G., Kawai U., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.O., Sakurai K., Satou M.,
RA Seki M., Shim P., Southwick A., Shinzaki K., Davis R.W., Ecker J.R.,
RA Theologis A.,
RT "Arabidopsis Full Length cDNA Clones."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY080658; AAL86334.1; -.
KW Hypothetical protein.
SQ SEQUENCE 311 AA; 33247 MW; SE3098B91F116BFD CRC64;

Alignment Scores:
Pred. No.: 5,096-25 Length: 311
Score: 398.50 Matches: 112
Percent Similarity: 53.33% Conservative: 40
Best Local Similarity: 39.30% Mismatch: 88
Query Match: 15.57% Indels: 45
DB: 10 Gaps: 12

US-09-935-124A-1 (1-1422) x Q8RXV3 (1-311)
Qy 426 GCGTATGTGCTGAGCGGAAGGCTGAGAGATGCGAGATGCCACGTCATCTG 485
Db 35 GlyTyr--AlaSerSerProGlyLysArgSerSerMetGluAspPheTyr-GluThrArg 53

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Qy 486 AAGACATCAGCCGAGAGTGAAGGCCCATCGTCCTCATTAATCGGTTTCATATTT 545
Db 54 IleAspGlyValGluGly-----GluIleValGlyLeuPhe 65
Qy 546 GCGTGTGTTGATGAGCATGAGAGAAATTCGAGCCTCAAAATTTGTGCGCAGAAATTTGCA 605
Db 66 GlyValPheAspGlyPheGlyGlyAlaArgAlaGluTyrValLysGlnAsnLeuPhe 85
Qy 606 CAAACTTAATCAGAAATTTCTTAAGAGATGTAAATCAGTGAAGAAACCGTGAAG 665
Db 86 SerAsnLeuIleArg--HisProLys-----PheIleSer-----AspThrThr 99
Qy 666 AGATGCTTTTGGACATCTTAAGCATATCTGATGAAGAGTTCTTAAACAGTTCCAGC 725
Db 100 AlaAlaIleAlaAspAlaTyrAsnGlnThrAspSerGluPheLeuLysSerGluAsnSer 119
Qy 726 CAGAAAGCTGCTGGAAAGAT--GGGTCCATGCGACGCTGTGTGTGGCTGTAGACAC 782
Db 120 GlnAsn-----ArgAspAlaGlySerThrAlaSerThrAlaIleLeuValGlyAsp 136
Qy 783 ATTCTTAATATTCGAACCTCGAGATAGTGGGCAATCTTGTGCTTAATATGAGAG 842
Db 137 ArgLeuLeuValAlaAsnValGlyAspSerArgAlaValIleCysArgGlyLysAsn-- 155
Qy 843 AGTCAAAACATGCAAGCTTAAGCCTCAGCAAGACATATCAATCACTAGATGAAG 902
Db 156 -----AlaIleAlaValSerArgAspHisLysProAspGlnSerAspGlu 170
Qy 903 CGGATGAGATACAGAGGCTGGAGAAAGCTCAGG-----GATGGGCGTGTGG 953
Db 171 ArgGlnArgIleGluAspAlaGlyGlyPheValMetTrpAlaGlyThrTrpArgValGly 190
Qy 954 GGGGCTGTAAGGTGTCAAGCTCCATTGGGGAGCGGGAGTACAAAGCCCTGGGTGACC 1013
Db 191 GlyValLeuAlaValSerArgAlaPheGlyAspLysLeuLeuLysGlnIleTyr--ValVal 209
Qy 1014 TCTGTGCCCCGACATCAGACGCTGCAGTGAACCCCAATGACAGTTTCATTTGTGGCC 1073
Db 210 AlaAspProGluIleGlnGluGluValValAspSerSerLeuGluPheLeuAla 229
Qy 1074 TGTGATGGCTCTTCAAGCTCTTAACTCCAGAGAAGCGGTGAACCTTCATCTGTCTGT 1133
Db 230 SerAspGlyLeuTrpAspValValThrAsnGluGluAlaValThrMetVal----- 1248
Qy 1134 CTCGAGAGTAAAGATCCAGACCCGGAGAGGAGATCGCGACGCCGCTACGAA 1193
Db 249 IleGluAspPro-----Glu 1253
Qy 1194 GCAGCTCGCAAGAGCTGGCCCAAGAGCGGTGCGAGCGGCTGCGCCAGCAAGCTACT 1253
Db 254 GluAlaAlaLysLysLeuMetGlnGlnAlaTyrGlnArgGlySerAlaAspAsnIleThr 273
Qy 1254 GTGATGTGTGTGCGG 1268
Db 274 CysValValValArg 278

RESULT 12
Q8S3P1 PRELIMINARY; PRT; 243 AA.
AC Q8S3P1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 26.7 kDa protein.
GN 24K23.16.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_Taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN=CV. NIPPONBARE;
 RA Park Y.-J., Rosetoks N., Ramakrishna W., Samiuel P., Shiloff B.,
 RA Ma J., Jiang Z., Kleinhofs A., Bennezen J.,
 RT "Sequence characterization of orthologous regions in the barley and
 RT rice genomes";
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AF480497; AAL87187.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 243 AA; 26734 MW; 8B481E1F559CE5F CRC64;

Alignment Scores:

Pred. No.:	9 526-24	Length:	243
Score:	383.00	Matches:	99
Percent Similarity:	53.96%	Conservative:	44
Best Local Similarity:	37.36%	Mismatches:	78
Query Match:	14.96%	Indels:	44
DB:	10	Gaps:	8

US-09-935-124A-1 (1-1422) x Q8R3P1 (1-243)

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QY 534 GTTTCATATTTTCTGTTTGTGATGAGACATGAGAAATTCGACCTCAAAATTTGCTGCA 593
DB 17 IIEGlyLeuphGlyValIheAepGlyHISGlyGlyAlaIyValaIaGluTyValIys 36
QY 594 CAGAAATTCGATCAAAACTTATACAGA-----AAATTTCTTAAAGAGATGTAACACT 647
DB 37 GlnAsnLeuphSerHisLeuLeuArgHisProLySpheIleSerAspThrIysValaIa 56
QY 648 GTAGAGAAAAACCGTGAAGAGATCCCTTTGGACACTTTCAGACATCTGATGAAAGCTTC 707
DB 57 ILeAsp-----AspAlaTyrlYsSerThrAspSerGluPhe 68
QY 708 CTTTAAACAAGCTTCCAGCAGAGAGCTGCGTGAAGAGATGGCTCACTGCTGCTGTT 767
DB 69 LeuGluSerAspSerSerGlnAsnGlnCys-----GlySerThrIAsSerThrAla 85
QY 768 CTGGCGCTGACACAACATTCTTATATTCGCAACCTCGAGATAGTCGGCAATCTTGTGT 827
DB 86 ValLeuValIGlyAspArgLeuphValaIaAsnValIGlyAspSerArgAlaIleIleCys 105
QY 828 CCTTATTAATGAGAGAGAGTCAAAAACATGCACCTTAAGCCTCGCAAAAGCATATACCA 887
DB 106 ArgGlyGlyAsn-----AlaIleAlaValSerIysAspHisIysPro 119
QY 888 ACTCAGTATGAGACGCGATGAGATACAGAAAGCTGAGAAAAGCTCAGG----- 938
DB 120 AspGlnThrAspGluArgGlnArgIleGluAspAlaGlyGlyPheValaIaMetTrpAlaGly 139
QY 939 GATGGCGCTGTTTGGCGCTGCTAGAGGTGTCAAGCTTCATTGGGAGCGGGCAGTACAA 998
DB 140 ThrTrpArgValIGlyGlyValaIaValaIaSerArgAlaPheGlyAspIysLeuLeuIys 159
QY 999 CGCTGCGGTGTCAACCTCTGTGCGCCGATCAGACGCTGCAGCTGACCCCAATGCAGG 1058
DB 160 GlnTyrlValaValaAsp--ProGluIleArgGluGluValaIleAspHisSerLeuGlu 178
QY 1059 TTCATTTTGTGGCTGTGATGGCTCTTCAAGGCTTTACCCCAAGAAAGCGCTGAC 1118
DB 179 PheLeuIleLeuAlaIaSerAspGlyLeuTrpAspValaIaThrAsnGluGluAlaValaIaAsp 198
QY 1119 TTCATCTTGTCTGTCTGACGATGAAAGATCCAGACCCGGAGAGGAAGTCCCGAGCC 1178
DB 199 MetThrArgSerIleHisAspProGluGlu----- 208
QY 1179 GACGCCCGCTACAGACACCTGCAACAGGCTGCGCAACAGCGCGGCTGCG 1238
DB 209 -----AlaAlaIySlySLeuLeuGlnGluAlaIyTrIysAspArgIys 222
QY 1239 GCCGACAACCTGCTGATGATGGTGTGATGAGGATGAGGCACTGAGCGGCGCGCAG 1298
DB 223 SerAspAsnIleThrCysValaIaValaIaArgPheLeuHis-----GlyGln 237
QY 1299 GAGCAGCATGTGTAT 1313

```

DB 238 GlySerSerGlyTyrl 242

RESULT 13

ID Q8RX37 PRELIMINARY; PRT; 380 AA.

AC Q8RX37 01-JUN-2002 (TRENBLrel. 21, Created)

DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TRENBLrel. 21, Last annotation update)

DE Hypothetical 40.7 kDa protein.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucosids II; Brassicales; Brassicaceae; Arabidops.

NCBI_TaxID=3702;

RA Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,

RA Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,

RA Tang C.C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,

RA Chen H., Cheuk R., Jones T., Karlin-Neumann G., Kim C., Lam B.,

RA Lin J., Meyers M.C., Miranda M., Nguyen M., Palm C.J., Shim P.,

RA Southwick A., Davis R.W., Ecker J.R., Theologis A.;

RT Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.

DR EMBL; AY090917; AAM13912.1; -.

KW Hypothetical protein.

SQ SEQUENCE 380 AA; 40709 MW; 7EA1DBB991F0E8BD CRC64;

Alignment Scores:

Pred. No.:	7e-23	Length:	380
Score:	373.50	Matches:	125
Percent Similarity:	42.20%	Conservative:	59
Best Local Similarity:	28.67%	Mismatches:	140
Query Match:	14.59%	Indels:	112
DB:	10	Gaps:	17

US-09-935-124A-1 (1-1422) x Q8RX37 (1-380)

```

QY 14 CTGCTCCGCCCGCCCGGGGGGTGTGAGCCCGCGCTGCGGGGCTGAG-----TGT 67
DB 41 LeuAsnProProValSerSerThrSerProSerAlaIaSerProThrSerProPheCys 60
QY 68 CTGTGCTGCTGCGCGCTCCACCGCCTCGGCATGAGACCTTCGGGAGCTGCGCGA 127
DB 61 LeuArgLeuLeuAspProProAlaIySLeuGlyPheGlySerAspSerGlyProIySer 80
QY 128 GCCCGAGCGCTGCGCGCGCCGCTGCGCGGAGAGAGAGCTCAGAAAGACCCCTGCTTT 187
DB 81 IleLeu-LysArgIySArgProThrThr----- 89
QY 188 TGATACCTCCCTCCGCGCAGACGACTGACTCAGAGATCAGGGGAGACCTTGTCTTTTGA 247
DB 90 -LeuAspIleProValaIa-----ProValGlyIleAlaIaProIleSerAsnAl 106
QY 248 TGATCTCCACCGCGCTAGACAGTGGGATTCAGGTTCTTGGCAATCAATATCCAGAT 307
DB 106 AspThrProArgIyGlu-----SerArgAl 115
QY 308 GGTAAAGCTGAAGGAGAGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 367
DB 115 aValIGluArgGluGlyAspGly----- 122
QY 368 TGAAGAGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 427
DB 123 -----TyrSerValTyrlCysIys----- 128
QY 428 CTAATGTGCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
DB 129 -----ArgGlyLySArgIyAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 143

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OY 905 GATAGATATACAGAGGCTGGAGAAAGCTCAGAGTGCGCTTTTGGCGGCTTGA 964
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 859 elysarlgvalthrlepleuylglymetillepheamhlguepnehgyserrleua 879
OY 965 GGTGTACGCTCATTTGGGAGCGGACAGTCAAGCCC-----TCCGCTGT 1009
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 879 avalsarlgserpnehglyaspllysglurylgluylgylvlypnehcys---- 897
OY 1010 CACCTCTGCGGACATACAGCTGCGACCTGACCCCAATGACAGTTTCATTTTGT 1069
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 898 -valseraprforyrglnthrthrthaspleuthrthalaargaphispherpelle 917
OY 1070 GGCCTGTGATGGCTCTTCAAGCTTTTACCCCAAGAAAGCCGTGAATTCATCTTGT 1129
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 917 ualacyasplglyleutrpaspllyvalgluryasplgluialaivalglnpheval----- 935
OY 1130 CTGTCTCGAGATGAAGATCCAGACCCGGAAGGAAATCCGACCGCCGCTTA 1189
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 936 -----GlnArgAmnillelysleuyllyserserlathrglu----- 947
OY 1190 CGAAGCAGCTGCAACAGGCTGCGCAACAGCGGTGCGAGCGGCTGCGCCGACACGT 1249
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 948 -----IlesergluleuleuAlaGlnAspserTyraAspArgIysserglYaspaAmn 965
OY 1250 CACTGTGATGGTGTG 1265
      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 965 ethrvalleuvalval 970

RESULT 16
QBVZD9 PRELIMINARY; PRT; 420 AA.
ID QBVZD9
AC QBVZD9;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DB AT5953140/MFH8.8.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koeseema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Murusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yemanux X., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Becker J.R.;
RT "Arabidopsis cDNA clones."; EMBL/GenBank/DBJ databases.
RU Submitted (NOV-2001) to the
DR EMBL; A1065026; AAL57666.1; -.
DR InterPro; IPR000222; P2C.
DR InterPro; IPR001932; P2C-like.
DR Pfam; PF00481; P2C; 1.
DR SMART; SM00332; P2C; 1.
DR SMART; SM00332; P2C; 1.
DR PROSITE; PS01032; P2C; UNKNOWN.1.
SQ SEQUENCE 420 AA; 45752 MW; 2DF6960D75BF9058 CRC64;

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Alignment Scores:
Pred. No.: 1,91e-22 Length: 420
Score: 368.50 Matches: 112
Percent Similarity: 50.44% Conservatve: 60
Best Local Similarity: 32.84% Mismatches: 108
Query Match: 14.39% Indels: 61
DB: 10 Gaps: 13

```

US-09-935-124a-1 (1-1422) x QBVZD9 (1-420)

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OY 291 ACATCATATCCAGATGTAAAGCTGAAGGAAAGCAAAAGAAAGAAACCTCCAG 350
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 Thrsrlalaysmethelvalaspthr-----serlalely 69
OY 351 GAAGAAGAAATGCACTGAAGACCTTGGAAGAAAGATTGTAAAGCTTCCTCGGTG 410
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 GlnuysarlgIleserleuvalasphmetProbiulysvalasphapdlylytrille 89
OY 411 ATCTTGCTGTGAAG-----GCTATGTGCTGAGCGGAG 446
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 90 gllygllylrylrylsasnasphaspllyserlseuercyselilyrlycysserhearg-- 108
OY 447 GGTGAAGAGGAGGAGATGCAAGGATGCCAGCTCATCTGAACACATCACCCAGAGAGTGT 506
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 109 GlynysarlgserThrmetglunaspheThraspllyleysalaserThrilleuily--- 127
OY 507 AGGCCCCCATGTCCTCATTACTCGGGTTTCATATTTGCTGCTTTTGTATGAGCATGA 566
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 128 -----GlnAlaValCyswerhegllylepheaspllyhilegly 140
OY 567 GGAATTCGAGCTCAAAATTTGCTGCAACAGAAATTCATCAAAATTCAGAAATTTT 626
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 141 Glyserlrglialaaglurlyleuylgyluhlsreuhemhenuewet---lyshis 159
OY 627 CCTAAGAGAGATATATCATGTGTAGAAAGACGTGAAGAGATGCTTTTGAAGCTTTC 686
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 160 Progin-----Pheleuthrasphthrlylsualaleuansgluthrtyr 174
OY 687 AAGCATCTGATGAAGATTCCTTAAACAGCTTCAGCCAGAACCTGCTCGAGAA--- 743
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 LysglthrtraspalalaleheleuIn-----serglunysaspthrtyrtyrtyr 191
OY 744 GATGGTTCACCTGCCAGCTGTGTGCTGTGAGCAAACTTTATATTCACCACTC 803
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 192 AsplgyserThrlyaserlalaValleuvalgllyasnhlsleuuryalalashval 211
OY 804 GGAAGTATGTCGGCAATCTTGTGTGTATATGAGAGAGTCAAAACATGCAACCTTA 863
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 212 GlynaspeirtrgThrilleval-----serlysalaglylsalalle 225
OY 864 AGCCTCAGCAAGACATATCCATCATCATGATGAGAGCGATGAGATCAGAGGCT 923
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 226 AlaleuaserasphslyserProasnargsersasplunrglyasrglilegluaserla 245
OY 924 GGAAGAAACGTCAAG-----GATGGGCTGTTTGGCGGTGTGAGATGTCACGC 974
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 Glyglyvalillemetrplalelythrtrparyalgllyvalleuulameterarg 265
OY 975 TCCATTTGGGAGGAGGAGACAGACAGCGCTGCGCTGCTGCTGCGACATCAGAGC 1034
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 266 Alaleuylasnmrgmetleuylslnphe---valvalaladubProbiulelalnsp 284
OY 1035 TGCAGCTGACCCCAATGACAGTTCATTTTGGCTGTGATGGCTTTCAGATC 1094
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 285 Leuqlulleasphlsglualagluleuvalleuulaseraspllyleutrpaspal 304
OY 1095 TTTACCCAGAGAGAGACCGGTGAATCTTCTGTCTGTCTGAGAGTAAAGATCCAG 1154
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 305 ValProasnglunspalaval-----AlaleuulalaglnserlunlunPro----- 320
OY 1155 ACCGGGAGAGGAAAGTCCGACCGCACCCCGCTACAGACAGCTGCAACAGCGTGGCC 1214
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 321 -----GlnAlaAlaAlaArglyseuThr 328
OY 1215 AACAAAGCGGTGACGCGGGCTCGGCCGACAACTGATGTGTGTGTGCGGATAGG 1274
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 329 AsphthrAlasaserarglyserlialasphamillethrcyslilevalalysphearg 348
OY 1275 CAC 1277
      |||
Db 349 His 349

RESULT 17

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RP SEQUENCE FROM N.A.
 RA Yamada K., Bahu J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 RA Deng J.M., Goldsmith A.D., Lee J.M., Onders C.S., Quach H.L.,
 RA Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
 RA Kaminici P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
 RA Kamiya A., Katlin-Neumann G., Kawal J., Kim C., Lam B., Lin J.,
 RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 RA Sakurai T., Satou M., Seki M., Shimizu P., Southwick A., Shinozaki K.,
 RA Davis R.W., Ecker J.R., Theologis A.,
 RT Arabidopsis Open Reading Frame (ORF) Clones."
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY045819; AAK76493.1; -
 DR InterPro: IPR000222; PP2C-
 DR InterPro: IPR001932; PP2C-like.
 DR Pfam: PF00481; PP2C_1.
 DR PROSITE: PS01032; PP2C; UNKNOWN 1.
 SQ SEQUENCE 420 AA; 45786 MW; C312D84D35159052 CRC64;

Alignment Scores:
 Pred. No.: 2.82e-22 Length: 420
 Score: 366.50 Matches: 112
 Percent Similarity: 50.15% Conservative: 59
 Best Local Similarity: 32.84% Mismatches: 109
 Query Match: 14.32% Indels: 61
 DB: Gaps: 13

US-09-935-124A-1 (1-1422) x Q94AT1 (1-420)

QY 291 ACATCAATATCCAGATGTTAAAGCTGAAGGAGAAAGAGAAAGAAACCTCCGAG 350
 DB 58 ThrsrAlaLysMetMetValAspThr-----SerAlaGly 69

QY 351 GAG 410
 DB 70 GluLysArgIleSerLeuValAspMetProGluLysValAspArgGlyGlyTyrIle 89

QY 411 ATCTTGGCTGAG-----GGCTATGCTGCTGAGAGAGAGAGAGAGAGAGAGAG 446
 DB 90 GlyGlyGlyTyrLysAsnAspArgGlySerLeuSerCysGlyTyrCysSerPheArg--- 108

QY 447 GGTGAG 506
 DB 109 GlyLysArgSerThrMetGluAspPheTyrAspIleLysAlaSerThrIleGluGly--- 127

QY 507 AGGCCCCATCGCTCCATTAACCTCGGCTTCAATTTTGGCTTTTGAAGAGAGAG 566
 DB 128 -----GlnAlaValCysMetPheGlyIlePheAspGlyIleGly 140

QY 567 GGAATTGAGCTCAAAATTTGCTGACAGAGATTGTCATCAAAACTTAACAGAAATTT 626
 DB 141 GlySerArgAlaIleGlyTyrLeuLysGluIleLysPheAsnAsnLeuMet---LysHis 159

QY 627 CCTAAGAGAGATGTAATCATCATGTAAGAGAAACCGTAGAGAGATGCTTTTGAACATTT 686
 DB 160 ProGln-----PheLeuThrAspThrLysLeuAlaLeuAsnGluThrTyr 174

QY 687 AAGCATATGATGAAGAGTCTCTTAACAAGAGCTTCCAGAGAGAGAGAGAGAGAG 743
 DB 175 LysGluThrAspValAlaPheLeuGlu-----SerGluLysAspThrTyrArgAsp 191

QY 744 GATGGTGCAGCTGACAGAGGCTTGTGCTGTAAGAGAGAGAGAGAGAGAGAGAGAG 803
 DB 192 AspGlySerThrAlaSerAlaValLeuValGlyAsnHisLeuTyrValAlaAsnVal 211

QY 804 GAGATATGTCGGGCAATCTGTGCTTATTAATGAAGAGAGAGAGAGAGAGAGAGAG 863
 DB 212 GlyAspSerHisThrIleVal-----SerLysAlaGlyLysAlaIle 225

QY 864 AGCTCAG 923
 DB 226 AlaLeuSerAspSerHisLysPheProAsnArgSerAspLysArgIleGluSerAla 245

QY 924 CGAGAGAAACCTCAG-----GATGGCGCTGTTTGGCGCTGCTGAGAGTGTACGC 974
 DB 246 GlyIleValIleLeuTyrAlaGlyThrTyrArgValGlyValLeuAlaMetSerArg 265

QY 975 TCCATTGGGAGCGGAGATGACAGAGCGCTGCGGTGTCACCTTGCCGACATCAGAGCG 1034
 DB 266 AlaPheGlyAsnArgMetLeuLysGlnPhe---ValValAlaLeuProGluIleGlnAsp 284

QY 1035 TGCCAGCTGACCCCGCATGACAGGTTCATTTTGGCTGCTGATGAGGCTCTCAAGGTC 1094
 DB 285 LeuGluIleAspHisGluLysIleLysLeuValLeuLysSerAspLysLeuTrpAspVal 304

QY 1095 TTTACCCGACAGAGAGCGGTGAATTTGCTGCTGCTGCTGAGAGATGAAGATCCAG 1154
 DB 305 ValProAsnGluAspAlaVal-----AlaLeuAlaIleSerGluIleLysPro----- 320

QY 1155 ACCCGGAG 1214
 DB 321 -----GlnAlaAlaAlaArgLysLeuThr 328

QY 1215 AACAGCGCTGACAGCGGCGCTGCGCCGACAGATCATGATGCTGCGCATAGAG 1274
 DB 329 AspThrAlaPheSerArgGlySerAlaAspAsnIleThrCysIleValValLysPheArg 348

QY 1275 CAC 1277
 DB 349 His 349

RESULT 19
 Q9UP70 PRELIMINARY; PRT; 757 AA.
 AC Q9UP70;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE KIA1072 protein.
 GN KIA1072.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN.
 BX MEDLINE=99397452; PubMed=10470851;
 RA Kikuno R., Nagase T., Ishikawa K., Hirogawa M., Miyajima N.,
 RA Tanaka A., Kotani H., Nomura N., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes. XIV.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro."
 RL DNA Res. 6:197-205 (1999).
 DR EMBL: AB028995; BAA83024.1; -
 DR HSSP: P35813; 1A6Q.
 DR InterPro: IPR000222; PP2C.
 DR InterPro: IPR001932; PP2C-like.
 DR Pfam: PF00481; PP2C; 1.
 DR SMART: SM00332; PP2C; 1.
 DR SMART: SM00331; PP2C StG; 1.
 DR PROSITE: PS01032; PP2C; 1.
 SQ SEQUENCE 757 AA; 84177 MW; 45593FC322FCBD3B CRC64;

Alignment Scores:
 Pred. No.: 3.43e-22 Length: 757
 Score: 366.50 Matches: 123
 Percent Similarity: 43.02% Conservative: 68
 Best Local Similarity: 27.70% Mismatches: 148
 Query Match: 14.32% Indels: 105
 DB: Gaps: 18

US-09-935-124A-1 (1-1422) x Q9UP70 (1-757)

QY 123 CCGAG 182


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Db      87 ProGluProGluGluGlu---AlaAlaValGluGluGluGluGluGluGluGluAla 105
Qy      183 CTCTTGAATGACCTCCCTCCGCGCAGAGTACTGATCAGATCAGGGGAGCTTTGCTT 242
Db      106 ThrAlaAlaAlaAlaProGluHisSerAlaValProPro-----ProProGlu 122
Qy      243 TTTGATGATCTCCACCC-----GCTACAGTGGC 212
Db      123 LeuProProLeuProProLeuProArgProLeuSerGluArgGleThrArgGluVal 142
Qy      273 GATTGAGTTCTCTTGCACATCATATCCAGATGGTAAAGCTGAA-----320
Db      143 GluGluGluSerLeuSerLeuSerLeuGluGluGluGluGluGluGluGluGluGlu 162
Qy      321 ---GGGAAAGAGCAAGAAAGAAAGAAAGCTCCGAGAA-----353
Db      163 LeuAlaAlaAlaLeuAlaArgAlaThrSerArgGluValLeuGluSerArgLeuSerAla 182
Qy      354 -----GAGAAAGAAATGGCACTGAAGACCTTGGAAAGAAAGTTTGTAA 398
Db      183 HisTyrIleProGluGluThrArgGlyThrGluGlyThrValGluIleGluThrVal 202
Qy      399 GCCTCTTCGGTATCTTTGCT-----CTGAGGGCTAT 431
Db      203 LeuAlaArgSerValPheSerIleLeuHisGluIleCysCysSerTyrValIleAspPhe 222
Qy      432 GTGGCTGAGCG-----AAGGCTGAG 452
Db      223 ProLeuAlaArgArgProGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 242
Qy      453 AGGGAGAGATGAGAGATGCGCCAGCTGATCTTGAAGCAATCAGCAGAGCTAGAGCCC 512
Db      243 ArgArgGluMetGluMetGluMetVal-----CysIlePro 254
Qy      513 CCATGCTCCCTCATTTCTGCGGCT-----TCATATTTTGTGTTT 554
Db      255 AspPheAspMetLeuPheAspLeuLeuGluValArgGluGluGluGluGluGluGluGlu 274
Qy      555 GATGACATGAGAGAAATTCGAGCCTCAAAATTTGTCGACAGAAATTTGTCACAAATTTA 614
Db      275 ArgGluHisGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 294
Qy      615 ATCGAAAA-----TTTCTTAAAGAGATGTAATGATGTGTAGAGAAAAGCTGAAAGAG 668
Db      295 ValArgGluGluMetPheProHisAspProAla-----Glu 306
Qy      669 TGGCTTTTGGACCTTGAAGCAATGATGAGATGCTTGAAGCAAGCTTCCAGCCAG 728
Db      307 AlaLeuSerValArgAlaPheArgValIleThrArgGluArgPheValGluValAlaAla 324
Qy      729 AAGCTGCTGGAAGAGATGGTCACTGSCACAGCTGTCTGCTGTAGACAACTTTCT 788
Db      325 ArgGluSerLeuArgCysGluGlyThrThrGluValValThrPheIleArgGluAspMetLeu 344
Qy      789 TATATTGCCAAGCTCGAAGATAGTCCGAGCAATTTGTCTGTTAATGAGAGAGACTCA 848
Db      345 HisValAlaIleTyrValGluArgSerGluValMetLeuValArg-----358
Qy      849 AAACATGAGCAAGCTTGAAGCTGACAGCAAGCAATTCACCAATGATGAGAGCGGATG 908
Db      359 LysGluGluGluAlaValGluMetLeuValProHisValArgProArgPheValGluGlu 378
Qy      909 AGGATGACAGAGCTGAGAGAAAGCTC-----AGGATGAGCGGTGTTTGGCGCTG 959
Db      379 ArgGluGluAlaLeuGluGlyCysValValIleThrPheGluAlaIleTyrArgValAsnGlySer 398
Qy      960 CTAGAGGTGTACAGCTTCATTTGGGAGCGGAGCAATCAAGCGC-----TGGGTGTACCC 1013
Db      399 LeuSerValSerArgAlaIleGluArgAlaGluHisIleValProTyrIleCysGluArgAla 418
Qy      1014 TCTGTCCCGGACATCAGAGCTCCAGCTCCAGCCCAAGCAAGCTTCATTTGTTGGCC 1073
Db      419 -----AspSerAlaSerThrValLeuArgGlyThrGluMetPyrLeuIleValAla 435

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Qy      1074 TGTGATGGGCTCTTCAAGGTCTTTACCCCAAGAAAGCCGTGAATCTTGTCTGT 1133
Db      436 CysArgGlyPheTyrAspThrValAsnProArgGluAlaValIleValVal-----452
Qy      1134 CTCGAGGATGAAAGATCCAGACCCGGAGAGGAAGTCCGCGACCGGCGCTTACGAA 1193
Db      453 -----SerAspHisLeuLysGluAsnAsnGlyAspSerSerMetValAla-----467
Qy      1194 GCAGCTTGCAACAGGCTGGCGCAACAAGAGCGGTGACAGCGGGGCTCGGCGCAAGCTACT 1253
Db      468 -----HisValLeuValAlaSerAlaArgAlaGlyIleSerSerAspAsnIleThr 484
Qy      1254 GTGATGTGTGTC 1265
Db      485 ValIleValVal 488

RESULT 20
ID      082469      PRELIMINARY;      PRT;      359 AA.
AC      082469;
DT      01-NOV-1998 (TREMBLrel. 08, Created)
DT      01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      Protein phosphatase-2C.
GN      PP2C.
OS      Mesembryanthemum crystallinum (Common ice plant).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
OX      NCBI_TaxID=3544;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=LEAF;
RX      MEDLINE=99200489; PubMed=10102366;
RA      Miyazaki S., Koga R., Bohmert H.U., Fukuhara T.;
RT      "Tissue- and environmental response-specific expression of 10 PP2C
RT      transcripts in Mesembryanthemum crystallinum.";
RL      Mol. Gen. Genet. 261:307-316(1999).
DR      EMBL; AF075580; AAC36698.1; -.
DR      HSRP; P35813; IACQ.
DR      InterPro; IPR000222; PP2C.
DR      InterPro; IPR001932; PP2C-like.
DR      Pfam; PF00481; PP2C; 1.
DR      SMART; SM00332; PP2Cc; 1.
DR      SMART; SM00331; PP2C_SIG; 1.
DR      PROSITE; PS01032; PP2C; 1.
SQ      SEQUENCE 359 AA; 39565 MW; 42CCBF092742CD6C CRC64;

Alignment Scores:
Pred. No.:      3,58e-22      Length:      359
Score:      365.00      Matches:      92
Percent Similarity:      52.25%      Conservative:      59
Best Local Similarity:      31.83%      Mismatches:      94
Query Match:      14.26%      Indels:      44
DB:      10      Gaps:      10

US-09-935-124A-1 (1-1422) x 082469 (1-359)
Qy      447 GGTGAGAGGAGAGATGAGATGCCACGTCATCTGAAAGACATCAGCAGAG--- 503
Db      58 GlyProArgLysTyrMetGluMetGluHisIleArgIleAspArgLeuSerValGluLeu 77
Qy      504 -----TGAGGCGCCCAATCGCTCCCATTTACTCGGGGTTTCATATTTGCT 548
Db      78 GlySerLeuPheArgCysArgProLysProSer-----AlaPheTyrGly 91
Qy      549 GTTTTGAATGACATGAGAGATTCAGACCTCAAAATTTGTCGACAGAAATTTGATCA 608
Db      92 ValPheArgGlyHisGlyGlySerGluAlaAlaIleTyrValArgGluAsnValMetArg 111
Qy      609 AACTTAATTCAGA-----AAATTTCTTAAAGG-----GATGTATCAGTGTAGG 653

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Db 112 PhepHePheGluAAspValSerPheProGluAlaSerGluLeuAAspGluLeuPheLeuGlu 131
Qy 654 AAACCGTGAAGAGATGGCTTTTGACACTTGAACCAATCACTGAAGAGAGCTCTTAAA 713
Db 132 ---GlyValGluAAsmCyValSerAlaArgAlaPhePheLeuAlaAsp-----LeuAla 147
Qy 714 CAAGCTTCCAGCCAGAACCTGCTGGGAAAGATGGTCCACTGGCCACTGTGTCTGGCT 773
Db 148 LeuAlaAspAspCySerSerIleSerThSerSerGlyThrThAlaLeuThAlaLeuVal 167
Qy 774 GTAGACACATTTCTTATATTGCCAACCTGGAGATAGTCGGGCAATCTTGTCCTTAT 833
Db 168 LeuGlyArgLeuLeuLeuValAlaAlaAlaGlyAspCyArgAlaValLeuCyArgGly 187
Qy 834 AATGAGAGAGTCMAAAACATGACCTTAAGCTCGACCAAGACATATATCCAACTCAG 893
Db 188 GlyGlu-----AlaIleAspMetSerGlnAspIleArgProThrTyr 201
Qy 894 TATGAGAGCGGATGAGATACAGAGCTGAGAGAAAGCTCAGGATGGCGGTGTTTG 953
Db 202 ProSerGluLysArgValGluGluLeuGlyGlyTyrValAspAspGlyTyrLeuAan 221
Qy 954 GCGGTGCTAGAGTGTACAGCTGCATTTGGGAGCGGAGCACTAAC----- 998
Db 222 GlyValLeuSerValSerAlaLeuGlyAspTyrAspMetLysLeuProLysGlySer 241
Qy 999 CGGTGGGTGTCACTCTGTGCGGACATAGACAGCTGCAGACTGACCCCAATGACAG 1058
Db 242 AlaSerProLeuIleSerGluProGluLeuArgGlnIleIleLeuThrGluAspAspGlu 261
Qy 1059 TTCAATTTTGTGGCTGTGATGGCTCTTCAAGCTTTTACCCCAAGAAAGCCGTGAC 1118
Db 262 PheLeuIleIleGlyCyAspAspGlyIleTyrAspValIleIleSerSerGlnGlnAlaValSer 281
Qy 1119 TTCATCTGTCTGTCTGAGAGATGAAAGATCCAGACCCGGGAAAGGAGACTCCGACCC 1178
Db 282 ILeVal-----ArgTyrGlyLeuLysArgHis 290
Qy 1179 GACCCCGCTACGAGCAGCTGCGACAGCGTGCACACAGCGCTGCAGCGGGCTCG 1238
Db 291 AspAspPro---GluGlnSerAlaLysAspLeuValAsnGluAlaLeuArgHis 309
Qy 1239 GCCGACACAGCTCACTGTATGATGATG 1265
Db 310 ILeAspAsnLeuThrValIleIleVal 318

RESULT 21
ID 08WY54 PRELIMINARY; PRT; 766 AA.
AC 08WY54:
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE P22CA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Wu G., Couch F.J.;
RT Five novel genes from 17q23 amplicon have different amplification and
RT overexpression frequency in breast cancer."
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF620269; AAF70325.1; -.
DR InterPro; IPR000222; P22C.
DR InterPro; IPR001932; P22C-1like.
DR Pfam; PF00481; P22C; 1.
DR SMART; SM00332; P22C; 1.
DR PROSITE; PS01032; P22C; 1.
SQ SEQUENCE 766 AA; 85242 MW; E79A909F3F01364B CRC64;

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Pred. No.: 4,61e-22 Length: 766
Score: 365.00 Matches: 122
Percent Similarity: 42.44% Conservative: 69
Best Local Similarity: 27.11% Mismatches: 151
Query Match: 14.26% Gaps: 108
Db: 4
US-09-935-124a-1 (1-1422) x 08WY54 (1-766)
Qy 123 CCGAGCCCGGAGCGCTCGCGCGCGCGCGCGGAGAAAGACTCAGAAAG----- 176
Db 87 ProGluProGluGluGlu-----AlaAlaValGluGlyGluGluGluGluGluAlaAla 105
Qy 177 -----CCCTGCTCTTGATGAC 194
Db 106 ThrAlaAlaAlaProGlyHisSerAlaValProProProProGluLeuProPro 125
Qy 195 CTCCCTCGGCGCAGCAGTACTGACTCAGAGATCAGAGGAGACCTTGCTTTGATGATCTC 254
Db 126 LeuProProLeuProArgProLeuSerGluArgIleThrProArgProLeuSerGluArg 145
Qy 225 CCACCCGCTAGCAGTGGCATTCAAGTCTCTTCCCATCATATATCCAGATGGTAAAG 314
Db 146 IleThrArgGluGluValGluGlyGluSerLeuAspLeuGluGlnGluGluGluGly 165
Qy 315 ACTGAA-----CGGAAAGACCAAGGAAAACTCCGAGGAA----- 353
Db 166 TyrAsnCyProSerPheLeuAlaAlaAlaLeuAlaArgAlaThrSerAspGluValLeu 185
Qy 354 -----GAGAAATGCGCATGACAGCTTGTG 380
Db 186 GlnSerAspLeuSerAlaHisTyrIleProLysGluThrAspGlyThrGluGlyThrVal 205
Qy 381 GAAAGAACTTTGTAAAGCTCTTGGGTGATCTTGTG----- 419
Db 206 GlnIleGluThrValLysLeuAlaArgSerValPheSerLysLeuHisGluIleCysCys 225
Qy 420 -----CTGAAGGCTATGTGCTGACGCG----- 443
Db 226 SerTyrValLysAspPheProLeuArgArgProGluLeuTyrTyrGluThrSerIle 245
Qy 444 -----AAGGTGAGGAGGAGGATGACAGATCCCACTCATCTGACAGCATC 494
Db 246 HisAlaIleLysAsnMetArgArgLysMetGluAspLysHisVal----- 260
Qy 495 ACCGAGAGTGTAGCGCCCATCGCCCTCATTACTCGGCT----- 536
Db 261 -----CysIleProAspPheAsnMetLeuPheAsnLeuGluAspGluGluGluGlu 277
Qy 537 TCATATTTGCTGTGTTTATATGAGATGAGAGATGAGCCCAAAATTGCTGCGACAG 596
Db 278 AlaTyrPheAlaValPheAspGlyHisIleGlyValAlaPheAlaIleTyrHisSerIle 297
Qy 597 AATTGCATCAAAACTTAATCAGAAA-----TTTCTTAAGAGATGTAAATCAGTGA 650
Db 298 HisLeuHisValAsnLeuValArgGlnIleMetPheProHisAspProAla----- 314
Qy 651 GAGAAACCGTGAAGAGATGCTTTTGACACTTCAAGCATCTGATGAAGAGTTCCTT 710
Db 315 -----GluAlaLeuCyAspArgAlaPheArgValThrAspGluArgGluVal 329
Qy 711 AAACAGCTTCCAGCCAGAAAGCTGCTCGAAGATGGGTCCACTGCCAGTGTCTCG 770
Db 330 GlnLysAlaAla-----ArgIleSerLeuArgGlySerIleThrThrGlyValValThrPhe 347
Qy 771 GCTGTAGACAAATCTTATATTGTCCAACCTCGAGATAGTGGGCAATCTTGTCGT 830
Db 348 IleArgGlyAsnMetLeuHisValAlaIleTyrValGlyAspSerGlnValMetLeuValArg 367
Qy 831 TATTAATGAGAGAGTCAAAACATGACACCTTAAGCTGACGAAAGAGCATATCAACT 890
Db 368 -----LysGlyGlnAlaValGluGluLeuMetLysSerProHisLysProAsp 381

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Alignment Scores:

Qy	891	CAGTATGAAGACCGAGTACAGATTCACAAAGGCTGAGGAAGACGTC-----AGGAT	941
Db	362	ArgGluAarGgGILuYvGILuAglIeGluAlaLeuGlyCySvIIeValITrPheGlyAla	401
Qy	942	GGGCGCTGTTTGGGCGGTCGTCAGAGGTGTACAGCTTCATTTGGGAGCGGACGTACAGCGC	1001
Db	402	TrpArgValaInaGlySerLeuSerValSerArgAlaIleGlyYAspAlaGluIuHieYsPro	421
Qy	1002	-----TGGGTGTACCTCTGTGTCGCCGACATCAAGACGCTGCACGCTGACCCCCAATAC	1055
Db	422	TyrIleCyvGILuYAspAla-----AspSerAlaSerThyValIleuYAspGlyThrGlu	438
Qy	1056	AGGTTCATTTGTTGGGCGCTGATGAGGCGCTCTCAAGGCTCTTAAACCGACAGAACGCGG	1115
Db	439	AspTyrIleuIleLeuAlaCyvAspGILyPheThyArgPThyValaInaProAspGluAlaVal	458
Qy	1116	AACTTCATCTTGTCTGCTCTCGAAGATGAAMAAGATCCAGACCCGGAGAGGAACTGCCCA	1175
Db	459	LyvAlaVal-----SerAspHisLeuIleGlyInaHnAmhILyAspSerSer	473
Qy	1176	GCCAGACGCCCTACGAAGACGCTGCACAGGCTGGCCAAAGCGGCTGACGGGGCC	1235
Db	474	MetValAla-----HisLyLeuValAlaIaSerXlaArgAspAlaGly	487
Qy	1236	TCGGCGCACAACGTCACTGTGATGTTGGTG	1265
Db	488	SerSerAspAsnIleThrValIleValVal	497
RESULT 22			
Q9LEW5		PRELIMINARY;	PRT; 348 AA.
AC	Q9LEW5		
DT	01-OCT-2000	(TrEMBLrel.15, Created)	
DT	01-OCT-2000	(TrEMBLrel.15, Last sequence update)	
DT	01-MAR-2002	(TrEMBLrel.20, Last annotation update)	
DE	Protein phosphatase 2C-like protein.		
GN	T3ON20.10.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eumustade II; Brassicales; Brassicaceae; Arabidopsi.		
OX	NCBI_TaxID=3702;		
RN	(1)		
RP	SEQUENCE FROM N.A.		
RA	Beyan M., Pereira S.A., van Staveren M., Dirkse W., Stiekema W.,		
RA	Barcoff I., Menez H.W., Ruid S., Lemke K., Meyer K.F.X.;		
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBD databases.		
RN	(2)		
RP	SEQUENCE FROM N.A.		
RA	EU Arabidopsis sequencing project;		
RL	Submitted (JUL-2000) to the EMBL/GenBank/DBD databases.		
DR	EMBL; AL365234; CAB96629.1;	-	
DR	HSSP; P35813;	1A6O.	
DR	InterPro; IPR001993;	Mitoch. carrier.	
DR	InterPro; IPR000222;	PP2C.	
DR	InterPro; IPR001933;	PP2C-like.	
DR	Pfam; PF00481;	PP2C.1.	
DR	SMART; SM00332;	PP2C SIG.1.	
DR	SMART; SM00331;	PP2C SIG.1.	
DR	PROSITE; PS00215;	MITOCH. CARRIER; UNKNOWN_1.	
DR	PROSITE; PS01032;	PP2C.1.	
QO	SEQUENCE	348 AA;	37379 MW; 12447BB07F740E2C CRC64;

Alignment Scores:	
Pred. No.:	3,96-22
Score:	364,50
Percent Similarity:	53,00%
Best Local Similarity:	36,40%
Query Match:	14,24%
DB:	10
US-09-935-124A-1 (1-1422) x Q9LEW5 (1-348)	
Length:	348
Matches:	193
Conservative:	47
Mismatches:	86
Indels:	47
Gaps:	13

Oy	426	GGCTATGTCGTGAGCGGAAGGGTGAAGGAGAGAAATCCAGAGT---	GCCACGCTATC	482
Db	35	gIyIyT---AlaserSerAlaGlyIyVaArgSerSerMetGluAspPhe	pheGluThrArg	53
Oy	483	CTGAACGACATCACCGAGAGTGAAGGCCCCATCGTCCCTCATTA	CTGAGGTTTCATAT	542
Db	54	IleAepGlyIleAenGlyGluIle-----ValGlyLeu	64	
Oy	543	TTTGCTGTTTTGATGGACATGTGAGGAATTCGAGCCTCAAAATTG	CTGCACAGAATTG	602
Db	65	pheGlyValPheAepGlyHisGlyIyAlaArgAlaAlaGlyTyrVal	IyVaArgHisIleu	84
Oy	603	CATCAAACTTAACAGAAAATTTCTTAAGAAGATGTAATCAGTGA	GTGAGAAAACCGTg	662
Db	85	PheSerAenLeuIle---ThrIAspProIys---PheIleSer---	AspThr	98
Oy	663	AAGAGATGCTCTTGGTGGACACTTTCAGACATCTAGATGAAGA	AGATTCCTTAAACAGCTTCC	722
Db	99	LySerSerAlaIleThrAapAlaTyrAenHisIleThrAapSerGlu	LeuLeuIySerGluAen	118
Oy	723	AGCCAGAAAGCCTGCTGGAAGAAT---GGGTCACTGTCACG	TGTGTCTGGCTGTAGAC	779
Db	119	SerHisAen-----ArgAapAlaGlySerThrAlaSerThrAla	IleLeuValGly	135
Oy	780	AACATCTTTATATATGGCAACCTCGAGAAATAGTCGGGGCAAT	CTGTGTGCGTATATAG	839
Db	136	AspArgLeuValValAlaAenValGlyAapSerAArgAlaValIle	SerArgGlyIyGlyIyS	155
Oy	840	GAGAGTCAAAAACATGACGCTTAAGCCTCAGCAAAAGACATTA	ATCCAACTGATGTGAA	899
Db	156	-----AlaIleAlaValSerArgAapHisIlyAspIleProAsp	IleSerAep	169
Oy	900	GAGCGATGAGGATACAGAAAGCTGTGAGAGAAACGTCAAGGA	TGGCGGTGTTTGGGCGTG	959
Db	170	GluAArgGluAArgIleGluAenAlaGlyIyGlyPheVal-----	MetTrpAlaGlyVal	186
Oy	960	CTAAGAGTGTACGCTCCATTTGGGAGCGGACGTAACAAGCGT	CGGCTGACCTCTGTG	1019
Db	187	LeuAlaValSerAArgAlaPheGlyAapAArgLeuLeuIyGlnTyr--	-ValValAlaAap	205
Oy	1020	CCGACATTCAGACGCTGCCAGCTGACCCCAATGACAGGTTCA	TTTGTTGGCTGTGAT	1079
Db	206	ProGluIleGlnGluGlyIyIleAapAapThrLeuGluPheLeuIle	uAlaIleuAlaSerAep	225
Oy	1080	GAGGCTTTCAAGGCTCTTTTACCACCAAGAAGACCGGTGA	CTTCACTTGTCTGTCTGAG	1139
Db	226	GlyLeuTrpAapValPheSerAenGluAlaAlaValAlaMetVal-	-----	240
Oy	1140	GATGAAAAGATCCAGACCGGGAAAGGAATCGCGACCGACG	CCGCTAGCAACAGACC	1199
Db	241	-----LysGluValGluAapPro-----GluAapSer	249	
Oy	1200	TGCACAAGCTGTGCGCAACAAGCGGTGACGCGGGCTCGGCG	CAACAAGTCACTGTGATg	1259
Db	250	AlaIyIySerIyIyValGlyIyAlaIleIyVaArgGlySerAlaA	pAaHisIleThrCysVal	269
Oy	1260	GTGTGTGGG	1268	
Db	270	ValValArg	272	
RESULT 23				
O9FXE4	1D	O9FXE4	PRELIMINARY,	PRT, 464 AA.
AC	O9FXE4,			
DT	01-MAR-2001	(T-EMBLrel. 16, Created)		
DT	01-MAR-2001	(T-EMBLrel. 16, Last sequence update)		
DT	01-MAR-2002	(T-EMBLrel. 20, Last annotation update)		
DE	FL1A21.5.			
OC	Amblydiparis thaliana (Mouse-ear cress).			
OC	Buxarivota; Vixridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsidae.			

RESULT	23
Q9FXE4	
ID	Q9FXE4
AC	Q9FXE4;
DT	01-MAR-2001 (T-EMBLrel. 16, Created)
DT	01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT	01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE	Fl2A21.5.
OS	Arabidopsis thaliana (Mouse-ear cress) .
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eudots II; Brassicales; Brassicaceae; Arabidopsids.
NCBI	Taxid=3702;

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RN [1]
SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA Shin P., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharzky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Becker J.R.;
"Genomic sequence for Arabidopsis thaliana BAC F12A21 from chromosome
1.";
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RA Becker J.R.;
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RA Becker J.R.;
RT Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A.
RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA Shin P., Altafi H., Bei B., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharzky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
RA Becker J.R.;
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
SEQUENCE FROM N.A.
RA Becker J.R.;
RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
SEQUENCE FROM N.A.
RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chlou J., Choi E.,
RA Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharzky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA Theologis A., Becker J.R.;
RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
EMBL: AC008113; MGC28911.1; -.
DR HSP: P35813; IAO.
DR InterPro: IPR00222; PF2C.
DR InterPro: IPR01352; PF2C-like.
DR Pfam: PF00481; PF2C.
DR SMART: SM00332; PF2C; 1.
DR SMART: SM00331; PF2C; SIG.
DR PROSITE: PS01032; PF2C; 1.
SQ SEQUENCE 464 AA; 51514 MW; EF210BDE7DBCBEE CRC64;

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QY 462 ATGAGATGAGCCAGCATCTGATGACAGCATCAGCAGAGAGATGAGGCGCCCATCTGC 521
DB 133 MetGluAspPheHisArgLysVal-----ProCysLeuValGlyAsnSer 147
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DB 148 -----LysLysSerPheGlyValValTyrSerPheGlyValValValValVal 164
QY 582 AAATTCCTGCACAGATTTGCATCAAACTTAATCAAGAAATTTCT-----AAAGCA 635
DB 165 GluPheValAlaGluLeuSerHisLysTyrValValAlaGluMetGluAsnCysLysGly 184
QY 636 GATGATATCATGTATGAGAAACCGTGAAGAGATGCTTTGGACACTTTCAGCATCAT 695
DB 185 LysGluGluLysValGlu-----AlaPheLysAlaAlaPheLeuArgThr 199
QY 696 GATGAGATGTTCTTAAACAGCTTCCAGCCAGAGAGCTGCTGGAAGATGGTCCACT 755
DB 200 AsparGlnPheLeuGluLysValLysGluGlnSerLeuLysGlyValValSerGly 219
QY 756 GCCACGTGTGTCTGCTGCTGTA-----GACAACATCTTTATTTGCGCAACCTCGAGAT 809
DB 220 AlaCysCysValThrValValLysGluGlnGluMetLysValSerHisLysGly 239
QY 810 AGTGGGCAATCTTGTGTCTTATATAGAGAGATGCAAAACATGACCTTAAAGCTTC 869
DB 240 CysArgAlaValLeuCysArgAlaGly-----ValAlaGluAlaLeu 253
QY 870 AGCAAGAGCATATATCAACTCATATGAGAGCGATGAGTACAGAG----- 920
DB 254 ThrAspAspHisLysProGlyArgAspAspGluLysGluLysGluSerGlnSerLeu 273
QY 921 -----GCTGAGAGAAACCTCAGGAT-----GGG 944
DB 274 IleProPheMetThrPheGlyLeuGlnGlyTyrValAspAsnHisGlnGlyValTyr 293
QY 945 CGTGTGTTGGCGCTGCTGAGAGGTGTCACGCTCCATTTGGGAGCGGAGATGACGCTGC 1004
DB 294 ArgValGlnGlyLeuAlaValSerArgSerIleGlyAspAlaHisLeuLysHis 312
QY 1005 GGTGCACCTCTGTGCTGACCATGACAGCTGCGACGTCGACCCCATATGACGTTTCAT 1064
DB 313 TrpValValAlaGluProGluThrArgValLeuGluGlnGluGlnAspMetGluPheLeu 332
QY 1065 TTGTGGCTGTGATGAGGCTTCAAGCTTTTCAAGCCCAAGAGACCGTGAATTCATC 1124
DB 333 ValLeuAlaSerAspGlyLeuThrAspValValSerAsnGlnGlnValValTyrThrVal 352
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DB 353 LeuHisValLeuAlaGlnArgLysThrProLysGluSerGluGlnGluAsnLeuValGln 372
QY 1155 -----ACCGGGAAGGG 1166
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QY 1190 ----- 1190
DB 413 ArgGluIleGlySerSerProSerLysSerProIleThrProTyrLysSerLeuTyrAla 432
QY 1191 GAAGAGCGCTGCAAGAGGTGCGCAAGAGCGGTGAGCGGGCTGCGCCAGCAACATC 1250
DB 433 LysAlaAlaCysLysGluLeuAlaAsnLeuAlaLysArgGlySerMetSerPhe 452
QY 1251 ACTGATGATGTCGCGGATGAGGAC 1277
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RESULT 24
ID 022200. PRELIMINARY; PRT; 404 AA.
AC 022200. (Tributylamine, 05, Created)
DT 01-JAN-1998 (Tributylamine, 05, Last sequence update)

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NCBI_Taxid=3702;
 RN [1]
 SEQUENCE FROM N.A.
 RA Yamada K., Barni J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
 RA Omidera C.S., Quach H.U., Tang C., Tortum M., Yamamura Y., Yu G.,
 RA Yu S., Bowser L., Carinci P., Chen H., Cheuk R., Hayashiaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
 RA Koeseema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shin P.,
 RA Southwick A., Tracy S.E., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Teologias A.;
 RT "Full Length cDNA of gene T20B5.6/At2g40860 (GI:2623300).";
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY056151; AL07230.1; -;
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR001932; P2C-like.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00481; P2C; 1.
 DR Pfam; PF00009; pkinase; 1.
 DR Prodom; PD000001; Euk_pkinase; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
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 SQ SEQUENCE 658 AA; 72852 MW; 66041EE6AEFE14 CMC64;

Alignment Scores:
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 DB 300 LysArgProSerSerAspAsnValValleuGluLeuGluSerIleTrpGluGlnValArg 319
 QY 156 GGGAGAGAGCTCAG 215
 DB 320 GILyLys-----GlnGlnGlnGlnLeuLeuGluLysThrSerAsnSerGlnSerAspThr 337
 QY 216 GACTCAGATCAGAGGAG 275
 DB 338 Asp-----GlyAlaAspIleIle-----LysAsnSerGlyAsp 348
 QY 276 TCAAGTTCTCTTCCACATCAATATCCAGATGTAAAGATGAGAGAGAGAGAGAGAG 335
 DB 349 TyrArgAspThrValAsnTrpPheSerGln-----GlyGluCysLeuSer 363
 QY 336 AG 395
 DB 364 LysLysSerSer----- 367
 QY 396 AAGAGCTTCGCTGATCTTTGCTGCTGATGAGGCTATGCTGAGAGAGAGAGAGAG 446
 DB 368 -----ValSerThrValPheAspValLysLeuTrpSerSerSerThrAspGluProSer 385
 QY 447 -----GTTGAG 464
 DB 386 ArgTyrValProValIleSerCysGlySerPheAlaThrCysGlyArgArgGluSerMet 405
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 QY 525 ATTACTCGAGTTTCATATTCTGCTGTTTGTGATGAGCATGAGAGAGAGAGAGAGAG 584

DB 419 ---GluSerIleHisleuPheAlaIlePheAspGlyHisArgGlyAlaAlaAlaGlu 437
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 QY 702 GAGTTCTTAACAGAGCTTCAGCCAGAGAGCTTCC-----TGG 740
 DB 469 AlaPheArgGlnGluLeuAspSerHisArgGlnSerArgValSerGlnLysAspTrp 488
 QY 741 AAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 800
 DB 489 HisProGlyCysThrAlaIleAlaSerLeuLeuValGluLeuLysLeuPheValAlaAsn 508
 QY 801 CTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 860
 DB 509 ValGlyAspSerArgAlaIleLeuGlyArgAlaGlyHis-----Pro 522
 QY 861 TTAGCCTCAGAGAGAGATTAATCACTCAGATGAGAGAGAGAGAGAGAGAGAGAGAG 920
 DB 523 PheAlaLeuSerIleAlaHisleuAlaThrCysIleAspGluArgAsnArgValIleGly 542
 QY 921 GCTGAG 965
 DB 543 GluGlyValArgIleGluTrpLeuValAspThrTrpArgValAlaProAlaGlyLeuGln 562
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 QY 1086 TTCAAGTCTTTATCCCAAG 1145
 DB 602 TrpAspValMetAsnAspGluGluValIleGlyIleIleArgAspThrValLysGluPro 621
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 DB 622 SerMetCysSerLys----- 626
 QY 1206 AGGCTGAGCAAG 1265
 DB 627 ArgLeuAlaThrGlnAlaAlaAlaArgGlySerGlyAspAsnIleThrValIleValVal 646

Search completed: February 9, 2003, 18:00:30
 Job time : 123 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: February 9, 2003, 17:51:10 / Search time 66 Seconds
(without alignments)
5741,890 Million cell updates/sec

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Perfect score: 2560
Sequence: 1 ggcacccagccgcgtcgtcgc.....ttttttccttaaaaaaaa 1422

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2199	85.9	441	AAU23566	Novel human enzyme
2	2199	85.9	446	AAU22933	Novel human enzyme
3	2143	83.7	421	ABR12317	Human protein phosphatase
4	2143	83.7	421	AA40555	Human polyprotein
5	2018	78.8	392	AA28791	Human hydroxylase-11
6	2018	78.8	392	ABR05726	Human signal transducer
7	2015	78.7	392	AA28585	Human protein segun
8	2014	78.7	392	AA43769	Human polyprotein
9	1457.5	56.9	378	ABG09377	Novel human diaphanous
10	1053	41.1	221	ABG09376	Novel human diaphanous
11	533.5	20.8	211	ABG07619	Novel human enzyme
12	518	20.2	138	AAU33252	Novel human enzyme
13	431.5	16.9	295	AAU38068	Arabidopsis thaliana
14	431.5	16.9	305	AAU38067	Arabidopsis thaliana
15	411	16.1	86	AAU38067	Human secreted protein
16	391.5	15.3	219	AAU38069	Arabidopsis thaliana
17	375.5	14.7	353	ABR77579	Physcomitrella patens
18	370.5	14.5	360	AAU38067	Arabidopsis thaliana
19	365.5	14.3	383	AAU38069	Arabidopsis thaliana
20	365.5	14.3	420	AAU38074	Arabidopsis thaliana
21	365.5	14.3	454	ABR08398	Arabidopsis thaliana
22	365.5	14.3	454	ABR08398	Human-derived protein
23	364	14.2	358	AAU38061	Arabidopsis thaliana
24	364	14.2	358	AAU38061	Arabidopsis thaliana
25	364	14.2	359	AAU38064	Arabidopsis thaliana
26	364	14.2	359	AAU38064	Arabidopsis thaliana
27	363	14.2	309	AAU38064	Arabidopsis thaliana
28	358.5	14.0	361	AAU38064	Arabidopsis thaliana
29	357.5	14.0	438	AAU38064	Arabidopsis thaliana
30	357.5	14.0	438	AAU38064	Arabidopsis thaliana
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33	352	13.8	434	AAU38064	Arabidopsis thaliana
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35	350	13.7	276	AAU38064	Arabidopsis thaliana
36	349	13.6	329	AAU38064	Arabidopsis thaliana
37	345.5	13.5	434	AAU38064	Arabidopsis thaliana
38	341.5	13.3	236	AAU38064	Arabidopsis thaliana
39	341	13.3	322	AAU38064	Arabidopsis thaliana
40	339	13.2	320	AAU38064	Arabidopsis thaliana
41	338.5	13.2	383	AAU38064	Arabidopsis thaliana
42	338	13.2	382	AAU38064	Arabidopsis thaliana
43	337.5	13.1	380	AAU38064	Arabidopsis thaliana
44	336	13.1	367	AAU38064	Arabidopsis thaliana
45	336	13.1	382	AAU38064	Arabidopsis thaliana
46	333	13.0	423	AAU38064	Arabidopsis thaliana
47	333	13.0	423	AAU38064	Arabidopsis thaliana
48	332.5	12.9	352	AAU38064	Arabidopsis thaliana
49	330.5	12.9	294	AAU38064	Arabidopsis thaliana
50	330	12.9	360	AAU38064	Arabidopsis thaliana

ALIGNMENTS

RESULT 1
ID AAU23566 standard; Protein; 441 AA.
AAU23566;
17-DEC-2001 (first entry)
Novel human enzyme polypeptide #652.
Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
ligase; hyperproliferative disorder; immunodeficiency disorder;
autoimmune disorder; neurological disorder; metabolic disorder;
inflammatory disorder; cardiovascular disorder; reproductive disorder;

KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX Homo sapiens.
XX OS
XX PN WO200155301-A2.
XX PD 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US01239.
XX PF
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
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PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251998.
PR 08-DEC-2000; 2000US-0251999.
PR 11-DEC-2000; 2000US-0254097.

PR	05-JAN-2001; 2001US-0259678.
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	Rosen CA, Barash SC, Ruben SM;
PI	WPI: 2001-465566/50.
XX	N-PSTDB: AAS41436.
DR	
XX	
PS	Claim 11; SEQ ID NO 1562; 1180bp; English.
XX	
CC	The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40781-AAS41694) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. influenza). The polynucleotides of the invention can also be used in gene therapy.
CC	AU22915-AU23814 represent the novel human enzyme polypeptides of the invention.
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC	
XX	
SO	Sequence 441 AA;
Alignment Scores:	
Pred. No.:	4,72e-218 Length: 441
Score:	2159.00 Matches: 423
Percent Similarity:	100.00% Conservatve: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	85.90% Indels: 0
DB:	Gaps: 0
US-09-935-124A-1 (1-1422) x AU235566 (1-441)	
OY	9 GCCCGCTGCTCCGCCGCCGGGTGTGAGACCCGCCGTGCTCGCGGCCTGAATGTC 68
Dd	19 AIAAGTGYCYSBAIProPfoCIyAlITperProAlaIalAIarGIyleuSerVal 38
OY	69 TGTGCTGCTCCGCCCTTCACACCAGACTCCGCCCTTGAGAACTTTGGGGAGACTCGCGAG 128
Dd	39 CYaAGTGYSCYBAIgtleuHTIProAlaSerAlaMetAspIeuPhgIIyaPleuProGlu 58
OY	129 CCGAGAGCGTGCAGCGGCCGCCGGTGCAGGAAAAGAAGCTCAAAAGAGCCCTTGCTTT 188
Dd	59 ProGUArgetserProAgtProAlaIalactIyleGluIdnILngILyglIProleuIeuPhe 78
OY	189 GAAGAGCTCCCTCCGGCGAGAGATATGAATCGAGATNAGAGGGAGACTTTGTTTAT 248
Dd	79 AspaApIeuProfoAlaSerSerThrasperdlISerclIGlyProleuIeuPheasp 98
OY	249 GATCTCCACCCGCTACAGATGGCATTAAGATTCTTTGGCAATCATMAATCCGATG 308
Dd	99 AspIeuProfoAlaSerSerThrasperdlISerIeuAlaTHSerIlIeserGlmetc 118
OY	309 GTAAAGACTGAAGGAAAGAGCAAGAAAAAACCTCCAGAGAAAGAGAAATGGCACT 368
Dd	119 ValVyrTHngILngILyglIyalaykrytgyrTHSerclIngILngILybaangIyser 138
OY	369 GAAGAGCTTGTGAAAAAGAAAGTTTGTAAAGCTCTTCGATCTTGTGTCTGAAGGC 428

Dd	139	GIUGLIULeuValGIuIuVlybVbAlCyElybAlaIseSerValIIlePheGlyLeuIuVsgIy	158
Qy	429	TATGCGCGTGAAGCGGAGAGCGGTGAAGAGAGATGACAGATATGCCACGTGATCCGTGAAC	488
Dd	159	TyValAlaGIuWgVlybGlyGIuWgGIuGIuWcGIuWcAlaIleValIIleuWen	178
Qy	489	GACATACCGAGAGAGGTGAAGGCCCCATATGTCCTCATTAATCGGGTTTCATATTTTGGT	548
Dd	179	AspIleIthGIuGIuCybAArgProIseSerIleuIIeIthArgValIseTyrPheAla	198
Qy	549	GTTTTTGATGACATGAGAGMATTCAGGCTCAAAATTTGCTGCACAAATTTGCATCA	608
Dd	199	ValPheAspGIyHIsGlyGIyIIleArgAlaIseTyrSPheAlaAlaGIuWcAlaIleuHIsGIn	218
Qy	609	AACTTAATACAGAAATTTCTTAAGAAGATGTAACTCACTGTAGAGAAAAACGTGAAGAGA	668
Dd	219	AsnIleuIIleArgVlybPheProVlybGIyAspValIIleIseValGIuVlybTyrValIlybArg	238
Qy	669	TGCGTTTTGGACACTTTCAGACATACCTGATGTGAAGAGTTCTTAAACAGGCTTCACCCAG	728
Dd	239	CyLeuIleuAspIthPheVlybHIsIthArgGIuGIuPheIuVlybGInAlaIseSerGIu	258
Qy	729	AAACCTGCTGGAAAGATGGGTCCATCGGCACAGTGTGTCCTGGCTGTGAACAATCTT	788
Dd	259	LysProAlaTPrVlybAspGIyIseThrAlaIthTyrVAlleuAlaValAspAsnIIleu	278
Qy	789	TATATTGCGCAACTCGGAGATATGTCGGGCAATCTTGTCCTTATATGAGAGACTCA	848
Dd	279	Ty-IIleAlaIleuIleGIyAspSerArgAlaIIleIleuCybArgTyrAsnGIuGIuIseGIu	298
Qy	849	AAACATGCGACCTTAAGCTCAGACAAAGAGCATATTCACATCGATGTGAAGCGCGATG	908
Dd	299	LysHIsAlaAlaIleuIseIleuSerIleuSerVlybGIuHIsAsnProthGIuIlyGIuGIuWcMet	318
Qy	909	AGGATTCACAAGCGTGAAGAAACGTCAAGGATGGCGGTTTTGGCGTGTGCTGAAGGTC	968
Dd	319	ArgIleGIuHlybAlaGIyGIyAsnValAspArgGIyAspValIleuGIyValIIleuGIuVal	338
Qy	969	TCACGCTCATATGGGAGACGGACAGTACAGCGCTCGGTGTCACTGTGCCCCGATC	1028
Dd	339	SerVlySerIleGIyAspGIyGIuIlybArgCybGIyValIthIseValIProAspIle	358
Qy	1029	AGACGTGTCACGCTGACCCCCCATATGACAGATTCAATTTTGTGGCTGTGATGGGCTCTTC	1088
Dd	359	ArgArgCybGIuIleuIthProAsnAspArgPheIIleIleuAlaIcybAspGIyLeuPhe	378
Qy	1089	AAAGTCTTATACCCCGAAGAGCCGTGAATCTTCATCTTGTCTCTGTCTCGAGATGAAGA	1148
Dd	379	LysValAlaPheThrProGIuGIuAlaValaIleAsnPheIIleuIseSerCybIeuGIuAspGIyIys	398
Qy	1149	ATCCAAACCCGGGAGAGGAAGTCCGACAGCGCAAGCCGCCCTTCAGAAAGACCTGCACAAG	1208
Dd	399	IIleGIuIthArgGIuGIyIyIseSerAlaAlaAspAlaArgTyrGIuAlaAlaIcybAsnArg	418
Qy	1209	CTGAGCCACAAGCGCGGTTCAGCGGGGCTCGGCGCAACAAGTCACTGTGATGTGTGGCG	1268
Dd	419	LeuAlaAsnIlybAlaValGIuArgIyIseSerAlaAspAsnValIthValMetValValArg	438
Qy	1269	ATGAGGGCAC 1277	
Dd	439	IIleGIyHIs 441	
RESULT 2			
AAU22933			
ID	AAU22933 standard; Protein; 446 AA.		
XX	AAU22933;		
XX	17-DEC-2001 (first entry)		
DT	Novel human enzyme polypeptide #19.		
DE			

PR 08-DEC-2000: 2000US-0251869.
PR 08-DEC-2000: 2000US-0251989.
PR 08-DEC-2000: 2000US-0251990.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0259678.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM,
XX WPI; 2001-465566/50.
DR N-PSDB; AAS40803.
XX
XX Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
PT diseases -
XX
XX Claim 11; SEQ ID No 929; 1180pt; English.
XX
XX The present invention relates to the isolation of novel human enzyme
CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders, including hyperproliferative disorders (e.g. cancer,
CC immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g.
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
CC blood-related disorders (e.g. haemophilia), reproductive disorders
CC (e.g. infertility) and infectious disorders (e.g. influenza). The
CC polynucleotides of the invention can also be used in gene therapy.
CC AAU22915-AAU23814 represent the novel human enzyme polypeptides of the
CC invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 446 AA:

Alignment Scores:
Pred. No.: 4,75e-218 Length: 446
Score: 2199.00 Matches: 423
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.90% Indels: 0
DB: 22 Gaps: 0

US-09-935-124A-1 (1-1422) x AAU22933 (1-446)

QY 9 GCCCGCTGCTGCGCCGCCCGCGGCTGTGAAGCCCGCGCTGCTCGCGGCTGAAGTTC 68
DB |||||||
DB 24 AATAGCGYCAATGProdiGlyValTrpSerProAlaAlaValGlyLeuSerVal 43
QY 69 TGTGCTGCTGCGCTTCACCCAGCCTTCGCCATGAGACTTTTGGGAGCTTCGCCGAG 128
DB |||||||
DB 44 CysATGCGYCAATGLeuAlaProAlaSerAlaMetAspLeuPheGlyAspLeuProGlu 63
QY 129 CCGAGCGCTCGCCCGCGCGCGCTGCCGAGAAAGACTCAGAAAGAGCCCTTCCTTT 188
DB |||||||
DB 64 ProGluArgSerProArgProAlaAlaGlyLeuGluAlaGlyLeuPhePhe 83
QY 189 GATGACCTTCCTCGCGCAGAGTACTGACTCAGAGTACGAGGGAGCTTTCCTTTGAT 248
DB |||||||
DB 84 AspAspLeuProProAlaSerSerThrAspSerGlySerGlyProLeuLeuPheAsp 103
QY 249 GATCTCCAGCCGCTAGAGAGTGGGATTCAGGTTCTTCGACCAATCAATTCACAGAT 308
DB |||||||
DB 104 AspLeuProProAlaSerSerGlyAspSerGlySerLeuAlaThrSerIleSerGlnMet 123
QY 309 GTAAAGCTGAAGGAAAGAGCAAAAGAAAAAAGCTCGAGAGAAAGAAAGATGCGCAT 368

DB 124 ValIysTrpGluGluValYsValAlaYsArgYsTrpSerGluGluGluValYsMetIleSer 143
QY 369 GAAAGCTTGTGAAAGAAAGATTGTAAAGCTTCTTCGTGATCTTTGTGTGAAGGCG 428
DB |||||||
DB 144 GluGluLeuValGluYsValYsValCysValYsAlaSerSerValIlePheGlyLeuYsGly 163
QY 429 TATGTGCTGAGCGGAGGCTGAGAGGAGAGATGACGAGTCCACGTCATCTCTGAAC 488
DB |||||||
DB 164 TyrValAlaGluArgYsGlyGluArgGluGluMetGlnAspAlaIleValIleLeuAsn 183
QY 489 GACATCACCGAGGAGTGTAGGCGCCCATCGTCCCTCATTACTCGGGTTTCATATTTGCT 548
DB |||||||
DB 194 AspIleThrGluGluCysArgProProSerSerLeuIleThrArgValSerTyrPheAla 203
QY 549 GTTTTATGATGACATGAGAAATTCAGACCTCAAAATTTCTGTACAGAAATTCATCA 608
DB |||||||
DB 204 ValPheAspGlyIleGlyIleArgAlaSerYsPheAlaIleGlnLeuMetIleGln 223
QY 609 AACTTAATCAGAAATTTCTTAAGAGATGTATTCGTGTAGAGAAACGCTGAAGGA 668
DB |||||||
DB 224 AsnLeuIleArgYsPheProYsGlyAspValIleSerValGluYsThrValYsArg 243
QY 669 TGCTTTTGGACACTTTCAGATCATCATGAAGTTCCTTAAGACTTCACGCGAG 728
DB |||||||
DB 244 CysLeuLeuAspTrpMetYsTrpMetIleGluGluGluGluGluGluGluGluGluGlu 263
QY 729 AAGCTGCTGGAAGAAATGGGTCCACTGCCAGTGTGTTTGCTGTAGACAACTTTCT 788
DB |||||||
DB 264 LysProAlaTrpYsAspIleYsThrAlaThrCysValLeuAlaValAspMetIleLeu 283
QY 789 TATATTCCAACTCCGAGATATGTCGGGCAATCTTGTGTGTATTAATGAGAGAGTCAA 848
DB |||||||
DB 284 TyrIleAlaAsnLeuIleYsPheArgAlaIleLeuYsArgTyrAsnGluIleSerGln 303
QY 849 AAACATCGACACTTAAGCTTCGACAAAGACATATCACTGATGATGAAGCGGATG 908
DB |||||||
DB 304 LysHisAlaAlaLeuSerLeuSerIleYsGluHisAsnProThrGlnTyrGluGluArgMet 323
QY 909 AGCATATCAGAAAGGCTGAGAGAAACGTACAGGATGGCGTGTGCGCTGACAGAGTG 968
DB |||||||
DB 324 ArgIleGlnYsAlaGlyGlyAsnValArgAspGlyArgValLeuGluValIleGluGluVal 343
QY 969 TCACGCTTCATTTGGGAGCGGAGCATGACAAAGCGCTGCGGTGTCCTGTGCGCAGATC 1028
DB |||||||
DB 344 SerArgSerIleGlyAspGlyGlnTyrTrpYsArgYsGlyValIleSerValProAspIle 363
QY 1029 AGAGCTGCGCAGCTGACCCGCAATGACAGTTCATTTGTGGCCCTGAGATGGGCTTC 1088
DB |||||||
DB 364 ArgArgCysGlnLeuMetProAsnMetArgPheIleLeuLeuAlaCysAspIleLeuPhe 383
QY 1089 AAGTCTTTTACCCCAAGAAAGCGGTGAATTCACTTGTCTGTCTGAGGATGAAG 1148
DB |||||||
DB 384 LysValIlePheThrProGluGluAlaValAsnPheIleLeuSerCysLeuGluAspIleYs 403
QY 1149 ATTCAGACCCGAGAAAGGAAATTCGCGACCGCGCTTACGAGACGCTTCGAAACGG 1208
DB |||||||
DB 404 IleGlnThrArgGluGluYsSerAlaIleAspAlaArgTyrGluAlaIleCysAsnArg 423
QY 1209 CTGCGCAACAGGCGGTGCGAGCGGGGCTCGGCCACAACTCATCTGTATGTGTGGCGG 1268
DB |||||||
DB 424 LeuAlaAsnYsAlaValGluArgGlySerAlaAspAsnValThrValMetValValArg 443
QY 1269 ATAGGCGAC 1277
DB |||||||
DB 444 IleGlyHis 446

RESULT 3
ID ABB12317 standard; peptide; 421 AA.
XX ABB12317;
XX

DT 11-JAN-2002 (first entry)

DE Human protein phosphatase 2C homologue, SEQ ID NO:2687.

XX

KM Human; cytokine; cell proliferation; cell differentiation; growth factor;

KM haematopoietic regulation; tissue growth; immunomodulator; activin;

KM inhibin; chemotaxis; chemokinesis; cancer; tumour; haematopoietic disorder;

KM myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

KM chronic inflammatory condition; proliferative retinopathy;

KM atherosclerosis; coronary heart disease; arterial ischaemia;

KM bone disorder; osteoporosis; vascular growth disorder;

KM tissue regeneration; wound healing; infection; immune disorder;

KM cell culture; drug screening; gene therapy; antiinflammatory;

KM antiaesthetic; antiarthritic; haemostatic; antiarteriosclerotic;

KM cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;

KM antifungal; vulnery; antitumor.

XX

OS Homo sapiens.

PN WO200157188-A2.

XX

PD 09-AUG-2001.

XX

PF 05-FEB-2001; 2001WO-US03800.

XX

PR 03-FEB-2000; 2000US-0496914.

XX

PR 27-APR-2000; 2000US-0560875.

XX

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-457740/49.

DR N-PSDB; ABA09561.

XX

PT Human proteins and DNA encoding sequences useful for preventing,

PT creating or ameliorating a medical condition in a mammalian subject

PT e.g. arthritis and cancer -

XX

PS Claim 20; Page 330; 1963jp; English.

XX

CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and

CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The

CC invention also relates to vectors and recombinant host cells comprising a

CC nucleotide of the invention, methods of producing the novel polypeptides,

CC antibodies against the polypeptides, methods of detecting the nucleotides

CC or polypeptides in a sample, and methods of identifying compounds which

CC bind to polypeptides of the invention. Although novel, many of the

CC polypeptides of the invention have homology to known proteins, thereby

CC giving an insight into their probable biological activities, and hence

CC potential therapeutic applications. The polypeptides of the invention may

CC have various activities, including cytokine, cell proliferation or cell

CC differentiation activities; stem cell growth factor activity;

CC haematopoietic regulatory activity; tissue growth activity;

CC immunomodulatory activity; activin- or inhibin-related activities;

CC chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC the invention are useful for preventing, creating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug

CC screening techniques. The present sequence represents a novel human

CC polypeptide of the invention.

XX

XX Sequence 421 AA;

XX

XX Alignment Scores:

XX Pred. No.: 2,84e-212 Length: 421

XX Score: 2143.00 Matches: 414

XX Percent Similarity: 100.00% Conservative: 0

XX Best Local Similarity: 100.00% Mismatches: 0

XX Query Match: 83.71% Indels: 0

XX DB: 22 Gaps: 0

XX

US-09-935-124A-1 (1-1422) x ABB12317 (1-421)

QY 36 TGAAGCCCGCGCGCTGCTCGCGGAGTGTCTGTGCTGCTGCGCGCTCCAGCCAGCC 95

DB 8 TTPSerProAlaAlaAlaArgGlyLeuSerValCySarGyCyArgLeuHtSPRoAla 27

QY 96 TCCGCCATGAGACCTCTTGCGGGGACCTGCCGAGCCCGAGCCGCTGCCGCCGCTGCC 155

DB 28 SerAlaMetAspLeuPheGlyAspLeuProGluProGluArgSerProArgProAlaAla 47

QY 156 GGGAAAGAAAGCTCAGAAAGAGACCCCTGCTTTGATGACCTCCCTCCGCGAGCACTACT 215

DB 48 GilyrSGlualaglnlybGlyProleuLeuPheAspAspLeuProProAlaSerSerThr 67

QY 216 GACTCAGATCGAGGGGAGACTTTGCTTTTGATGATCTCCACCCGCTAGCAGTGGCAT 275

DB 68 AspSerGlySerGlyGlyProleuLeuPheAspAspLeuProProAlaSerSerGlyAsp 87

QY 276 TCAAGTCTCTTGCCACATCATATCCAGATGTAAAGACTGAAGGAGAAAGACCAAG 335

DB 88 SerGlySerLeuAlaThrSerLeSerGlnMetValLySThGluGlybGlyAlaLyS 107

QY 336 AGAAAAACCTCCGAGAGAGAGAAAGATGGCAGTGAAGACTGTGGAAGAAAGAAAGTTGT 395

DB 108 ArgLySThSerGluGlnGlnLybAsnGlySerGlnGlnLeuValGlnLybLySValCyS 127

QY 396 AAAGCCTCTTCGAGTATCTTTGCTGAAGGGCTATGTGCTGACCGAGAGGGTGAAGAG 455

DB 128 LySAlaSerSerValIlePheGlyLeuLySgLyTyValAlaGluArgLybGlyGlnArg 147

QY 456 GAGGAGATGACAGATGCCACCTCATCTGAAACGACATCACCGAGAGATGTAGGCCCTCA 515

DB 148 GluGlnMetGlnAspAlaHisValIleLeuAsnAspIleThGluGlnCySarArgProPro 167

QY 516 TCGTCCCTCATACTCGGGGTTTCATATTTTGGCTTTTGGATGACATGAGAGAAATTCGA 575

DB 168 SerSerLeuIleThArgValSerTyRheaAlaValPheAspGlyHisGlyGlyLeArg 187

QY 576 GCCTCAAAATTTGTCGACAGAAATTTGCATCAAACTTAATCAGAAATTTGCTTAAGA 635

DB 188 AlaSerLySPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLybPheProLySgLy 207

QY 636 GATGTAATCAGTGTGAGAGAAACCTGGAAGATGCTTTTGGACATTTCAAGCATACT 695

DB 208 AspValIleSerValGlnLybThrValLybArgCybLeuLeuAspThrPheLybHisThr 227

QY 696 GATGAAGAGTTCTTAACAAGCTTCAGCAGCAGAGCCTGCGTGAAGAATGGGTCACAT 755

DB 228 AspGluGlnPheLeuLybGlnAlaSerSerGlnLybSPRoAlaATPlybAspGlySerThr 247

QY 756 GCCAGTGTGTCTGCTGTGAGACAACATTTCTTATTTGCGCAACTCGAGATAGTCGG 815

DB 248 AlathrCybValLeuAlaValAspAsnIleLeuTyRleAlaAsnLeuGlyAspSerArg 267

QY 816 GCATCTTGTGTGTTATTAATGAGAGAGTCAAAAACATGCAGCTTAAAGCTTCAGCAA 875

Db 268 AlaIleLeuCyArgTyrAsnGluGluSerGlnLysRhlAAlaIleLeuSerLeuSerLys 287
QY 876 GAGCATATATCAACTCACTATATGAAAGCGAGATGAGAGATACAGAAAGCTGAGAAACGTC 935
Db 288 GIuHtIsaSnProThrGlnTyrGluGluArgMetArgIleGlnLysAlaGlyGlyAsnVal 307
QY 936 AGGAGTGGGCGCTGTTTGGGCGCTGCTAGAGTGTCAAGCTCCATCGGAGGAGGAGCAGTAC 995
Db 308 ArgAspGlyArgValLeuGlyValLeuGluValSerArgSerIleGlyAspGlyGlnTyr 327
QY 996 AACGCTGGGCTGTCACCTCTGTGTCGCCGATCAAGCTGTCACCTGACCCCAATGAC 1055
Db 328 LysArgCysGlyValThrSerValProAspIleArgTyrCysGlnLeuThrProAsnAsp 347
QY 1056 AGGTTCATTTTGTGGCGCTGAGAGGCTTCAAGCTTTCACCCGAAAGGAGCGCG 1115
Db 348 ArgPheIleLeuLeuAlaCysAspGlyLeuPheValIlePheThrProGluGluAlaVal 367
QY 1116 AACTTCATCTTGTCTCTGTCGAGATGAAAAGATCCAGACCCGGGAAAGGAGTCCGCA 1175
Db 368 AsnPheIleLeuSerCysLeuGluAspGluLysIleGlnThrArgGlyGlySerAla 387
QY 1176 GCCGACGCCCTTACGAAAGACCTTGCAACAGCTGAGCAACAGGCGGTGCAGCGGAGC 1235
Db 388 AlaAspAlaArgTyrGluAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgGly 407
QY 1236 TCGGCGGACAGACGTCACCTGTGATGTGTGTCGGATAGGCGAC 1277
Db 408 SerAlaAspAsnValThrValMetValValArgIleGlyHis 421
RESULT 4
ID AAM40555 standard; Protein; 421 AA.
XX AAM40555;
AC XX
XX AAM40555;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5486.
XX
XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; chromolytic; drug screening; arthritis; inflammation;
XX leukemia.
XX
OS Homo sapiens.
XX
XX
PN W0200153312-A1.
XX
PD 26-JUL-2001.
XX
XX 26-DEC-2000; 2000MO-US34263.
PF
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0683036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
PI Tang YT, Liu C, Aunudi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Weinman R, Xu C, Xue AU, Yang Y, Zhang J;
PI Zhao QH, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX
XX N-PSDB; AA157111.

PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
PS
XX
XX Example 2; SEQ ID NO 5486; 10078pp; English.
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nocotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilization of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukemia and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 421 AA;
XX
Alignment Scores:
Pred. No.: 2,846-212 Length: 421
Score: 2143.00 Matches: 414
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 83.71% Indels: 0
Dels: 22 Gaps: 0
US-09-935-124A-1 (1-1422) x AAM40555 (1-421)
QY 36 TGSAGCCGCGCGCTGCTGCGGGGCTGAGTGTGCTGCTGCTGCGGCTCCACCCAGC 95
Db 8 TtpserProAlaAlaAlaArgIlyLeuSerValCysArgCysArgSerLeuHisProAla 27
QY 96 TCGGCGATGAGACCTCTTGGGGGAGCTGCGGAGCGGAGGCTGCGCGCGCGCTGCC 155
Db 28 SerAlaThrAspLeuPheIleGlyAspLeuProGluArgSerProAlaAla 47
QY 156 GCGAAAGAACCTCAAGAAAGACCCCTGCTTTGATGACCTCCCTCCGCGCAGCATCT 215
Db 48 GlyLysGluAlaGlnLysGlyProLeuLeuPheAspLeuProAlaSerSerThr 67
QY 216 GACTGAGATCAGGGGAGCTTTGCTTTTGATGATCTCCACCGCTNAGCATGCGCAT 275
Db 68 AsperGlySerGlyGlyProLeuLeuPheAspLeuProAlaSerSerGlyAsp 87
QY 276 TCAAGTCTCTTCCACATCAATATCCAGATGTAAAGACTGAAGGAAAGCAAG 335
Db 88 SerGlySerLeuAlaThrSerIleSerGlnMetValIleThrGluGlyLysGlyAlaLys 107
QY 336 AGAAAAACCTCCGAGGAAGAAGAAATGCGAGAGCTTGGAAGAAAGATTGTT 395
Db 108 ArgIleThrSerGluGluGluLysAsnGlySerGluGluLeuValGluLysValLys 127
QY 396 AAAGCTCTTCGGTATCTTTGCTGTAAGGGCTATGCTGAGGAGGAGGAGGAGGAGG 455
Db 128 LysIleSerSerValIlePheGlyLeuLysGlyLysValAlaGluLysGlyLysValArg 147
QY 456 GAGGAGATGAGAGATGCCAGCTCATCTGAAAGCACTCAAGGAGAGTGGCCCCCA 515
Db 148 GluGluMetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluGlyArgProPro 167
QY 516 TCGTCCCTCTTACTCGGCTTTCATATTTTGTCTTTTGTATGAGATGAGAGATTGGA 575
Db 168 SerSerLeuIleThrArgValSerTyrPheAlaIlePheAspIlyHisGlyLysIleArg 187
QY 576 GCTTCAAAATTTGCTGCACAGAAATTTGCATCAAAATTAACTGAAAAATTTCTTAAAG 635
Db 188 AlaSerLysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGly 207

QY	636	GATGTAATCAAGTGTGAGGAAACCCGTGAAGAAGATGCCCTTTTGACACTTTCAAGACTACT	693
Db	208	AspValIleSerValIGluIysThrValLysArgCysLeuLeuAspThrPheIysHisThr	227
QY	696	GATGAAGAGTCCCTTAACAAGAGCTTCCAGCGACAGAGCGCTCCGGAAGAGATGGGTCACT	755
Db	228	AspGluGluPheLeuLeuGlnIleAspIleSerGlnIlyPheProIleTyrIleAspIlySerThr	247
QY	756	GCCACGTGTGTTTGGCGCTGTGAGCAACATTTCTTATATATGGCAACCTCGAGATAGTCGG	815
Db	248	AlaThrCysValLeuAlaValAlaAspAsnIleLeuTyrIleAlaAsnLeuCllyAspSerArg	267
QY	816	GCAATCTTGTCGTCCGTATTAATGAGAGAGTCGAAAAATGACAGCTTAAAGCTTCAGCGAA	875
Db	268	AlaIleLeuCysAsArgIYrAsnGluGlnIleSerGlnIlyHisAlaAlaLeuSerIleuSerIys	287
QY	876	GAGCATATTCACACTCAGTATGAAAGACGGATGAGGATACAGAGGTCAGAGGAGAAACGTC	935
Db	288	GluHisAsnProThrGlnTyrGluGluIlyAsnMetArgIleGlnIlyAsnAlaGlyIlyAsnVal	307
QY	936	AGGGATGGCGCTGTGTTTGGCGGTGTGAGAGTGTCAAGCTTCACATTGGGGACGGGCAATAC	995
Db	308	ArgAspArgIyArgValLeuGluIyValLeuGluIlyValSerArgSerIleGlyAspGlyIlyThr	327
QY	996	AAGCGCTGGCGGTGTCACTCTGTGTGCCGAGATATAGACGCTGCCAGCTGACCCCCAATAC	1055
Db	328	LysAsnGlyCysGlyIyValIlyThrSerValProAspIleArgArgCysGlnIleuThrProAsnAsp	347
QY	1056	AGGTTCAATTTGTTGGCCTGTGATGGGCTTTTCAAGAGTCTTTAAACCCAGAAAGACCGGTG	1115
Db	348	ArgPheIleLeuLeuAlaCysAspGlyLeuPheIyValPheThrProGluGluAlaVal	367
QY	1116	AACTTCATCTTGTCTCTGTCTTCAGAGATGAAAGATCCCAAGCCCGGAGAGGAAAGTCCGCA	1175
Db	368	AsnPheIleLeuSerCysLeuGluAspGluIlyIleGlnThrArgGluIyIySerAla	387
QY	1176	GCCGACGCCGCGCTCAAGAGACGCTGCAAGAGCGTGGCCCAAGAGCGGTGACGGGGGC	1235
Db	388	AlaAspAlaAsArgIYrGluAlaAlaCysAsnArgLeuAlaAsnIlyValAlaGlnIlyArgGly	407
QY	1236	TGGGCGGACAACTCACTGTGATGGTGGTCCGATAGGGCAC	1277
Db	408	SerAlaAspAsnValThrValMetValValArgIleGlyHis	421
RESULT 5			
XX	ID	AAAB28791	
AC	AAAB28791	standard; Protein; 392 AA.	
XX	XX	AAAB28791;	
XX	XX	13-FEB-2001 (first entry)	
DE	XX	Human hydrolase-like molecule 2 protein.	
KW	XX	Hydrolase-like molecule; human; cell proliferation disorder;	
KW	XX	autoimmune; cancer; AIDS; acquired immune deficiency syndrome.	
OS	XX	Homo sapiens.	
OS	XX	US6132964-A.	
XX	XX	17-OCT-2000.	
XX	XX	06-FEB-1998; 98US-0013881.	
XX	XX	06-FEB-1998; 98US-0013881.	
XX	XX	(INCY-) INCYTE PHARM INC.	
XX	XX	Bandman, O, Hillman JL, Guegler KJ, Shah P, Lal P, Corley NC;	
XX	XX	WPI; 2001-006133/01.	

DR	N-F8DB; AAC60224.
XX	
XX	New human hydrolase-like molecules (HHLMs) and polynucleotides encoding
PT	the HHLMs, useful for diagnosing, treating or preventing cell
PT	proliferation (e.g. bone cancer) or autoimmune disorders (e.g. AIDS or
PT	asthma) -
XX	
PS	Claim 1; Column 43-46; 38pp; English.
XX	
CC	The present invention relates to isolated and purified cDNA encoding a
CC	human hydrolase-like molecule (HHLM), designated HHLM-1 to HHLM-8. The
CC	HHLM DNAs and polypeptides are useful for diagnosing, treating or
CC	preventing cell proliferation disorders and autoimmune disorders. Cell
CC	proliferation disorders include cancers, autoimmune disorders include
CC	AIDS (acquired immune deficiency syndrome). The present sequence
CC	is a HHLM protein of the invention.

SQ Sequence 392 AA;

Alignment Scores:

Pred. No.:	2.31e-199	Length:	392
Score:	2018.00	Matches:	3922

Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match:	78.83%	Indels:	0
DB:	22	Gaps:	0

US-09-935-124A-1 (1-1422) x AAB28791 (1-392)

102 ATGAGCCCTTCGAGGACCTGACCGGAGCCCGAAGCGCTCGGCGGCGGCGGCTGCGCGGAAA 161

1 Met Aant'leu Phag' vAant'leu Brog' i' Brog' i' uarns a e Bro' a' r' a' Bro' a' a' i' a' g' i' v' i' vs 20

[illegible][illegible][illegible][illegible]

41 GlySerGlyCysProLeuLeuPheAspAspLeuProProAlaSerSerGlyAspSerGly 60

282 TCTCTTGCACATCAAAATCCAGATGGTAAAGACTGAAGGGAAAGGACCAAGAGAAAA 341

Db 61 SerLeuAlaThrSerIleSerGlnMetValIysThrGlnGlyLysGlyAlaLysArgLys 80

Qy 342 ACCTCCGAGGAGAGAGATGGCAGTGAAGCTTGTGGAAGAAAGATTGTAAAGCC 401

Db 81 ThrSerGluGluGluLysAsnGlySerGluGluLeuValGluLysValCysLysAla 100

Qy 402 TCTTCGGTATCTTTGCTGTAAGGGCTATATGTGGCTGACGGGAAGGCTGAGAGGAGAG 461

Db 101 SerserValIlePheGlyLeuLysGlyTyrValAlaGluArgLysGlyGluArgGluGlu 120

462 ATGCAGATGCCACGTCATCTGAACGACATCACCGAGAGTGTAGGCCCATCGTCC 521

Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCysArgProProSerSer 140

QY 522 CTCATTACTCGGGTTTCATATTTTGCCTGTTTTTGATGACATGGAGGAATTCAGCCTCA 581

Db 141 LeuIleThrArgValSerTyrPheAlaValPheAspGlyHisGlyIleArgAlaSer 160

582 AAATTTCGTGCACAGAAATTTGCATCAAACTTAATCAGAAATTTCCCTAAAGAGATGTA 641

Db 161 LysPheH1A1AGlnAsnLeuH1GlnAsnLeu1LeuArgLysPheProLysG1LysAspVal 180

642 ATCAGTCGAGAGAAAACCGTGAAGAGATGCCTTTTGGACACTTCAAGCATACTGATGAA 701

Db 181 ILeSerValGluLysThrValLysArgCysLeuLeuAspThrPheLysHisThrArgGlu 2000

QY 702 GAGTTCCTTAACAAGCTTCCAGCCAGAGCCTGCTCGAAAGATGGGTCCACTGCCACG 761

Db 201 GluPheLeuLysGln]aSerSerGlnLysPro]a]aTProLysAspGlySerThrAlaThr 220

QY 762 TGTGTCGCTGATGACAACTTTTATTTCCCACTCGGAGATGTCGGGCATC 821
DB 221 CysValLeuAlaValAspAsnIleuNyrIleAlaAsnLeuGlyAspSerArgAlaIle 240
QY 822 TTGTGTCGTTATATAGAGAGATCAAAAATCATGACGCTTAAAGCTTCAGCAAGAGCAT 881
DB 241 LeuCysArgTyrAsnGluGluSerGlnLysHlaIleAlaLeuSerLeuSerLysGluHla 260
QY 882 AATCAACTCAGTATGAAGACGCGATGAGATACAGAAAGCTGAGAAACGTACGAGAT 941
DB 261 AspProThrGlnTyrGluGluArgMetArgIleGlnLysAlaGlyLysAsnValArgAsp 280
QY 942 GGGCGTGTGTTGGGGGCTGAGAGTGTCAAGCTCCATTCGGGAGCGGCGAGTCAACAGCG 1001
DB 281 GlyArgValLeuGlyValLeuGluValSerArgSerIleGlyAspGlyGlnTyrLysArg 300
QY 1002 TGGGAGTACCTCTGTGTCGCGGAGATCAAGCGTGCACGTGACCCCAATGACAGGTTG 1061
DB 301 CysGlyValIleThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
QY 1062 ATTTGTGGCTGTGATGGGCTGTCAAGCTCTTAAACCCGAGAAAGCCGTGAAGTTC 1121
DB 321 IleuLeuAlaCysAspIleuNyrLeuValPheThrProGluGluAlaValAsnPhe 340
QY 1122 ATCTGTCTCTGTCTGAGATGAAAGATCCAGACCGGAGAGGAGATCCGACGCGAC 1181
DB 341 IleuSerCysLeuGluAspIleuLysIleGlnThrArgGlyLysSerAlaAlaAsp 360
QY 1182 GCCCGCTACGAAGACCTTGCAACAGGCTGCGCAACAGGCGGTGACGCGGCTCGGCC 1241
DB 361 AlaArgTyrGluAlaIleCysAsnArgLeuAlaAsnLysAlaValaGlnArgLysSerAla 380
QY 1242 GACACGCTACTGTGATGTGTGTCGAGTACGAGGAC 1277
DB 381 AspAsnValIleThrValMetValValaArgIleGlyHis 392
RESULT 6
ID ABB05726 standard; Protein; 392 AA.
XX ABB05726;
AC ABB05726;
XX 30-APR-2002 (first entry)
DT 30-APR-2002 (first entry)
XX Human signal transduction protein clone tes3_31j20.
DE Human signal transduction protein clone tes3_31j20.
XX Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
KM gene therapy.
XX Homo sapiens.
OS Homo sapiens.
XX WO200198454-A2.
PN WO200198454-A2.
XX 27-DEC-2001.
PD 27-DEC-2001.
XX 25-APR-2001; 2001WO-1B02050.
PF 25-APR-2001; 2001WO-1B02050.
XX 25-APR-2000; 2000US-199380P.
PR 25-APR-2000; 2000US-199380P.
XX (GENU-) GERMAN HUMAN GENOME PROJECT.
PA (GENU-) GERMAN HUMAN GENOME PROJECT.
PI Wiemann S;
XX WPI: 2002-055660/07.
DR N-PSDB; ABA93763.
XX Human cDNA sequences and clones derived from human fetal brain, fetal
PT kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
PT screening and therapy -
XX Claim 1; Page 377; 61pp; English.
PS The present invention describes assemblages and computer readable media
CC

CC comprising novel human cDNA sequences and clones derived from human
CC foetal brain, foetal kidney, melanoma, testis and amygdala cDNA
CC libraries. ABA93702 to ABA93766 represent human cDNA sequences from the
CC present invention which encode the proteins given in ABB05662 to
CC ABB05729. The human cDNA sequences and clones can be used in gene
CC therapy. The clones may be used in a variety of applications, for
CC example they may be used in profiling assays, for providing large arrays
CC of human genetic material for implementing large-scale screening
CC strategies and for treating diseases via gene therapy procedures.
XX
SQ Sequence 392 AA;
Alignment Scores:
Pred. No.: 2,31e-199 Length: 392
Score: 2018.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.83% Indels: 0
DB: 23 Gaps: 0
US-09-935-124A-1 (1-1422) x ABB05726 (1-392)
QY 102 ATGACCTCTTCCGGGACCTGCCGAGCCGAGCGCTCCGCCGCGCTCCGGGAAA 161
DB 1 MetAspLeuPheGlyAspLeuProGluProGluArgSerProAlaIleGlyLys 20
QY 162 GAACCTCAAGAGACCCCTGCTCTTTGATGACCTCCCTCCGCGCAGCATGACTCA 221
DB 21 GlnLaglnLysGlyProLeuLeuPheAspLeuProProAlaSerSerThrAspSer 40
QY 222 GGATCAGGGGAGACCTTGTCTTTTGTGATGATCTCCACCCGCTAGCAGTGGCATTCAGGT 281
DB 41 GlySerGlyLysProLeuLeuPheAspLeuProProAlaSerSerThrAspSer 60
QY 282 TCTCTGCCCATCATATATCCAGATGCTAAGACTAAGAGCAAGAGCAAGAGAAA 341
DB 61 SerLeuAlaThrSerIleSerGlnMetValIleThrGluGlyLysGlyAlaLysArgLys 80
QY 342 ACCCGCAGAGAAAGAGAAATGCGAGTGAAGCTTGTGAAAAGAAATTTGTAAGCC 401
DB 81 ThrSerGlnGlnLysAsnLysSerGlnLysValaGlnLysValaCysLysAla 100
QY 402 TCTTCGGGTATCTTGTGCTGAGAGGCTAAGGCTGAGAGGCTGAGAGAGAG 461
DB 101 SerSerValIlePheGlyLeuLysGlyTyrValaAlaGlnLysGlyLysValaGlnLys 120
QY 462 ATGAGAGATCCCACTCATCTTGAACGACATCCGAGAGGTGAGGCCCATGCTCC 521
DB 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGlnCysArgProProSerSer 140
QY 522 CTCATTACTCGGCTTTCATATTTTCTGTTTGTATGACATGAGAGAAATTCGACCTCA 581
DB 141 LeuIleThrArgValSerTyrPheAlaValaPheAspGlyHisGlyGlyLysArgLys 160
QY 582 AAATTTGCTGCACAGAAATTTGATCAAAATTAATCAGAAATTTCTTAAGAGATGTA 641
DB 161 LysPheAlaIleGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
QY 642 ATCAGTGAAGAAACCGTGAAGAGATGCTTTTGAACCTTCAAGCATCTGATGAA 701
DB 181 IleSerValGlnLysThrValLysArgCysLeuLeuAspThrPheLysHisThrAspLys 200
QY 702 GAGTTCCTTAAAGACCTTCCGAGAGGCTGCTGAGAGAGAGTGGCTCACTGCGCAG 761
DB 201 GluPheLeuLysGlnLysSerSerGlnLysProAlaIleTyrAspGlySerThrAlaThr 220
QY 762 TGTGTCGCTATATAGAGAGATCAAAATCATGACGCTTAAAGCTTCAGCAAGAGCAT 821
DB 221 CysValLeuAlaValAspAsnIleuNyrIleAlaAsnLeuLysAspSerArgAlaIle 240
QY 822 TTGTGTCGTTATATAGAGAGATCAAAAATCATGACGCTTAAAGCTTCAGCAAGAGCAT 881
DB 241 LeuCysArgTyrAsnGluGluSerGlnLysHlaIleAlaLeuSerLeuSerLysGluHla 260

Qy	882	AATCCAACTCAAGTATGAAGAAGCGGATGAAGATACAGAAGGCTGGAGGAACCTCAAGGAT	941
Db	261	AenProthrGlnTrgIuGluAArgMeCargIleGlnIuYsaIaGlyYsaValIArgasp	280
Qy	942	GGGGGTGTTTGGGGCGTCAAGAGGTGTCAAGCTCCATTTGGGGAGGGGGAGTACAAAGGC	1001
Db	281	GlyArgValIleuGlyValIleGluIuValSerArgSerIleGlyYsaPoiYlnTrpYsaArg	300
Qy	1002	TGCGGTGCACCTCTGTGCCGACATCAGACGCTGCAGCTGACCCCAATGACAGATTTC	1061
Db	301	CysGlyValTruSerValProAspIleArgArgCysGlnIuNeuThrProAsnAspArgPhe	320
Qy	1062	ATTTTGTTGGGCTGTGATGGGCTCTTCAAGCTCTTTACCCCAAGAGAACCGTGAATCTTC	1121
Db	321	IleuLeuAlaCysAspArgIleuPheIuValPheThrProGluIuIuIaValAsnPhe	340
Qy	1122	ATCTGTGCTCTCTCGAGGAGTGAAGAATCCACAGCCGGGAGGGAGATGCCACCGAC	1181
Db	341	IleuSerCysIeuGluIuAspGluIuValIleGlnThrArgGluIuYsSerIaIaAsp	360
Qy	1182	GCCCGTACGAAGACGCTTGCAACAGGCTGGCCCAAGAGCGGTGCAAGCGGGGCTCGGCC	1241
Db	361	AlaArgTrgIuIuIaIaIaCysAsnArgIuLeuIaAsnIuYsaIaValGlnArgIuYserIa	380
Qy	1242	GACAACTGCTACTGTGATGTGTGTGTCGGAGTATGGGCAAC	1277
Db	381	AspAsnValTruValMetValIaArgIleGlyIHis	392

the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13528 and AAH13533 to AAH18742 represent human cDNA sequences; AAB522446 to AAB58593 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

the complementary strand of a polynucleotide which comprises one of

Db 201 GIuPheLeuYsGInAlaSeSerGInLYsPfoAlaTrpLYsAspGlySerThrAlaThr 220
QY 762 TGTGTTTGGCTGTAGACACATTTCTTATATATTCACACCTCGAGATAGTCGGGCAATC 821
PI 221 CyValLeuAlaValAspAsnIleLeuTrpIleAlaAsnLeuGlyAspSerArgAlaIle 240
XX 822 TTGTGCTGTTATATAGAGAGATCAAAAACATGCAGCCTTAAAGCTTCAGCAAGAGCAT 881
Db 241 LeuCyArgTrpAsnGluGluSerGInLYsIleAlaIleLeuSerLeuSerLYsGluHis 260
QY 882 AATCCAACTCAGTATGAGAGAGCGGATGAGATACAGAGCTGAGAGAAAACGTACGGCAT 941
PI 261 AsnProThrGInLYsGluGluArgMetArgIleGInLYsAlaGlyAsnValArgAsp 280
QY 942 GGGCGTGTGTTGGGGGCTGTAGAGTGTACAGCTCATTGGGGAGCGGCAATGACAGCGC 1001
Db 281 GYAArgValLeuGlyValLeuGluValSerArgSerIleGlyAspGlyGInLYsArg 300
QY 1002 TGGGTTGACCTGTGTCGCGGACATACAGCGTGCACCTACCCCAATGACAGCTTC 1061
Db 301 CyGlyValThrSerValProAspIleArgArgCyGInLYsGInLYsProAsnAspArgPhe 320
QY 1062 ATTTTGTGGCTGTGATGGCTCTTCAAGGCTTTTACCCCAAGAAAGCCGTGAACCTTC 1121
Db 321 IleLeuLeuAlaCyAspGlyLeuPheLYsValPheThrProGluGluAlaValAsnPhe 340
QY 1122 ATCTGTCTGTCTCGAGAGATGAAAAGATCCAGACCCGGAGAGGAGTCCGACGCGAC 1181
Db 341 IleLeuSerCyLeuGluAspGluLYsIleGInLYsArgGluGlyLYsSerAlaAlaAsp 360
QY 1182 GCCCGTACGAGCAGCAGCTGCAACAGCGCTGGCCACAGCGGCTGACGGGGCTCGGCC 1241
Db 361 AlArgTrpGluAlaAlaCyAsnArgLeuAlaAsnLYsAlaValGInLYsArgGlySerAla 380
QY 1242 GACACGTCAGTGTGATGATGATGTCGGATGAGGAC 1277
Db 381 AspAsnValThrValMetValValArgIleGlyHis 392

RESULT 8
AAM38769
ID AAM38769 standard; Protein; 392 AA.
XX AC AAM38769;
XX DT 22-OCT-2001 (first entry)
XX DS Human polypeptide SEQ ID NO 1914.
XX KW Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX OS Homo sapiens.
XX PN NC020015312-A1.
XX PD 26-JUL-2001.
XX PE 26-DEC-2000; 2000MO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSB-) HYSBQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanec RP;
XX WPI: 2001-442253/47.
DR N-PSDB; AA157925.
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX Example 3; SEQ ID NO 1914; 10078bp; English.
XX PS The invention relates to human nucleic acids (AA157798-AA161369) and
XX CC the encoded polypeptides (AAM38642-AAM42213) with noctropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localized neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilization of the activity, chemotactic/chemokinetic activity, haemostatic
XX CC activity/inhibin activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemia and
XX CC C.N.S disorders.
XX CC Note: The sequence data for this patent did not form part of the printed
XX CC specification.
XX SQ Sequence 392 AA;
XX Alignment Scores:
XX Pred. No.: 5,986-199 Length: 392
XX Score: 2014.00 Matches: 391
XX Percent Similarity: 100.00% Conservative: 1
XX Best Local Similarity: 99.74% Mismatches: 0
XX Query Match: 78.67% Indels: 0
XX DB: 22 Gaps: 0
US-09-935-124A-1 (1-1422) x AAM38769 (1-392)
QY 102 ATGACCTCTTTGGGGGACCTGCGGAGCCGAGCCGCTCGCGGCGCGGCGGAGAA 161
Db 1 MetAspLeuPheGlyAspLeuProGluProGluTrpSerProArgProAlaIleLYs 20
QY 162 GAACTCAGAAAGACCCCTGCTCTTTGATGACCTCCCTCGGCCAGCAGTACTGATCA 221
Db 21 GluAlaGInLYsGlyProLeuLeuPheAspAspLeuProAlaSerSerThrAspSer 40
QY 222 GGATCAGGGGAGACCTTTGCTTTTATGATGATCTCCACCGCTAGCAGTGGCATTCAGGT 281
Db 41 GlySerGlyGlyProLeuLeuPheAspAspLeuProProAlaSerSerGlyAspSerGly 60
QY 282 TCTCTGCGCACATCAATATCCAGATGCTAAAGACTAAGAGGAAAGAGCAAGAGAAA 341
Db 61 SerLeuAlaThrSerIleSerIleSerGInLYsThrGInLYsGlyAlaLYsArgLYs 80
QY 342 ACCTCGAGAGAGAGAAAGATGAGCAGTGAAGGCTGTGAGAAAAGATTTGTAAACC 401
Db 81 ThrSerGluGluGluLYsAsnGlySerGluLeuValGluLYsValCysLYsAla 100
QY 402 TCTTCGAGATCTTTGCTGTAAGGCTATGTCGCTAGCGGAGGAGGAGAGAG 461
Db 101 SerSerValIlePheGlyLeuLYsGlyTrpValAlaGluArgLYsGlyGluArgGluGlu 120
QY 462 ATGACAGATGCGCAGCTGATCTCTGAACGACATGCGAGAGAGTGTAGGCCCATCTGCC 521
Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCysArgProProSerSer 140
QY 522 CTCATTACTGGGTTTCATATTTTCTGTTTGTATGATGACATGAGAGAAATTCAGCCTCA 581
Db 141 LeuIleThrArgValSerTrpPheAlaValPheAspIlyHisGlyGlyIleArgAlaSer 160

QY 312 AAGACTGAAGGAAAGAGCAAAAGAAAACTCCGAGAGAGAGAAATGGCACTGAA 371
 CC |||||
 CC 108 LyeThrglUGlyysgdlYalysaRgLyThrsErglUGlulYsaenglYsErglu 127
 CC |||||
 QY 372 GAGCTTGCGAAAGAAAGTTTAAAGCCTCTTCGGTATCTTTGGTCTGAAGGGCTAT 431
 CC |||||
 CC 128 GluleuValGlulYalYsValCysLysAlaSerSerValIlePhgEglYeuYsGlyTyr 147
 CC |||||
 QY 432 GTGGCTAGACGGAAGGGTGAAGAGAGATGCAGATGCCACCTCATCTCGAAGCAG 491
 CC |||||
 CC 148 ValAlaGluArgLysGlyLysGluArgGluGluMeGlnPhaIstValIleLeuAenAap 167
 CC |||||
 QY 492 ATCACCAGAGAGTGAAGCCCCCATGCTCCCTCATTAATCTCGGGTTTCATATTTGCTGT 551
 CC |||||
 CC 168 IleThrglUGlucYsaRgProPseSerSerLeuIleThrArgValSerTyrPheAlaVal 187
 CC |||||
 QY 552 TTGTGAGCAGTGAAGAAATTCAGCTCAAAATTTGCTGCACAGAAATTTGCTCAAAAC 611
 CC |||||
 CC 188 PheAspGlyHlsGlyGlyIleArgAlaSerLysPheAlaIleGlnAenHlsGlnAen 207
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 QY 612 TTAATCAGAAAAATTTCTTAAAGAGATGTATCAGTGTAGAG 653
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 ID ABG07619 standard; Protein; 211 AA.
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 AC ABG07619;
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 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #7610.
 XX
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KM food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI: 2001-639362/73.
 DR N-PSDB; AAS71806.
 XX
 PT New isolated polynucleotide and encoded polypeptide, useful in
 PT diagnostic, forensic, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID No 37978; 103bp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPD
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 211 AA;

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US-09-935-124A-1 (1-1422) x ABG07619 (1-211)

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 QY 918 AAGGCTGAGGAAAGCTGACGAGGAGGCTGTTGGGGGCTGCTAGAGGTGCAGCCTCC 977
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 QY 978 ATTGGGAGCGGCGAGTACAGCGCTGCGGTGTCACCTGTGTCGCCGAGATCAGACGCTGC 1037
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 QY 1155 ACCCGGAAAGGAGATCCGACGCCGCGCTACGAGACAGCTGCAACAGCGTGGCC 1214
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 QY 1215 AACAAAGCGGTGACAGCGGGCTCG--GCCGACAACGTCACTGTATGGTGGTGGGAGTA 1271
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 AAU23252
 ID AAU23252 standard; Protein; 138 AA.
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 AC AAU23252;

XX 18-DEC-2001 (first entry)
XX Novel human enzyme polypeptide #338.
XX Human: oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
OS Homo sapiens.
PN WC200155301-A2.
XX 02-AUG-2001.
PD 17-JUN-2001; 2001WO-US01239.
PF 31-JAN-2000; 2000US-0179065.
XX 04-FEB-2000; 2000US-0180628.
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US-09-935-124A-1 (1-1422) x AAG18068 (1-295)

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xx Protein identification; signal transduction pathway; metabolic pathway;
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX 06-SEP-2000.
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PR 01-SEP-1999; 99US-0151930.

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PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
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Score: 431.50 Matches: 102
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Best Local Similarity: 37.23% Mismatches: 86
Query Match: 16.86% Indels: 27
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US-09-935-124A-1 (1-1422) x AAG18067 (1-305)

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Db 54 ArgGluAlaGluGluAspLysPheSerPheValSerGluGlyLysGluPheLeuVal 73
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QY 423 AAGAGCTATGTGCTGACCGAAGAGGTGAGAGAGATGCAGATGCCACAGTATC 482
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Db 74 GluAlaAspValAlaGluAspLysGlyAlaArgHisThrMetGluAspValTTPValVal 93
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QY 483 CTGAGCAGATCACCAGAGAGTGAAGCCCCCATCGCTCCATTAATCGGGTTTCATAT 542
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QY 543 TTGGCTGTTTGTGATGAGACATGAGAGAAATTGAGCCTCAAAATTGTCGACAGAAATTG 602

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Alignment Scores:

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Pred. No.: 2,63e-31 Length: 219
Score: 391.50 Matches: 84
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Best Local Similarity: 38.01% Mismatches: 65
Query Match: 15.29% Indels: 17
DB: Gaps: 6

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US-09-935-124A-1 (1-1422) x AAG18069 (1-219)

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QY 522 CTCATTACTCGGGTTTCATATTTGCTTTTGTGATGACGAGAGAAATTCAGGCTCA 581
DB 19 Leu-----ArgCysAlaHisPheAlaIleTyrAspGlyHisGlyIleArgLeuAlaIa 36
QY 582 AATTTGCTGCACAGAAATTTGCATCAAACTTATCATGAGAAATTTCTTAAAGAGATGTA 641
DB 37 GluPheAlaLysLeuHisLeuHisLeuAsnValLeuSerAlaGlyLeuProArgGluLeu 56
QY 642 ATCAGTGAAGAAACCTGAAAGAGATGCTTTTGACACTTTCAGACATCTAGTAA 701
DB 57 LeuAspVal---LysValAlaLysLysAlaIleLeuGluGlyPheArgLysThrAspGlu 75
QY 702 GAGTTCCTTAAACAGCTCCAGCCAGAACCTGCTGAAAGATGGTCCACTGCCACG 761
DB 76 LeuLeuLeuGluHisLysSerValSer-----GlyGlyIleuGluAspIleValAlaThrAlaVal 93
QY 762 TGTGTTCTGCTGTGAGACAACATCTTTATATGACCACTCGAGAGATGTCGGGCAATC 821
DB 94 CysValIleuIleuAspGlnLysValIleuValAlaAsnIleGlyLysAspAlaLysAlaVal 113
QY 822 TTGTGTCGT-----TATATGAGAGAGATCAAAAAACAT 854
DB 114 LeuAlaArgSerSerThrThrAsnGluLeuGlyAsnHisThrGluHisLysAsnProLeu 133
QY 855 GAGGCTTAAAGCTCAGCAAGAGCATATCCAACTCAGTATGAGAGAGGAGTGAAGATA 914
DB 134 LysAlaIleValLeuThrArgGluHisLysAlaIleTyrProGlnGluArgSerArgIle 153

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QY 972 CGCTCATTTGGGAGCGGACAGTACAGCGCTGCTGCTGTGTGCTGCCACATTCAGA 1031
DB 174 ArgAlaPheGlyLysAspArgHisPheLysLysPheGlyValSerAlaThrProAspIleHis 193
QY 1032 CGCTGCAGCTGACCCCAATGACAGGTTTCATTTGTTGGCTGTGATGAGGCTTTCAG 1091
DB 194 AlaPheGluLeuThrGluArgGluAsnPheMetIleLeuGlyCysAspIleuTrpGlu 213
QY 1092 GTC 1094
DB 214 Val 214
RESULT 17
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ID ABR77579 standard; Protein, 353 AA.
AC ABR77579;
DT 02-SEP-2002 (first entry)
DE Physcomitrella patens PP2C-1 SEQ ID NO 14.
KW Physcomitrella patens; PHSRP; phosphatase stress related protein;
PP2A; PP2C; enzyme; transgenic; plant; stress tolerance.
OS Physcomitrella patens.
XX WO200246442-A2.
XX 13-JUN-2002.
XX 06-APR-2001; 2001WO-US11253.
XX 07-APR-2000; 2000US-196001P.
XX (BADI ) BASF PLANT SCI GMBH.
XX Da Costa ESO, Bohmert HJ, Ishitani M, Van Thielén N, Chan R;
XX WPI; 2002-508562/54.
XX N-PSDB; ABR81333.
XX New transgenic plant cell transformed by phosphatase stress-related
XX protein coding nucleic acid whose expression in the cell results in
XX increased tolerance to environmental stress compared to wild type cell
XX -
XX Claim 16; Fig 3; 106pp; English.
XX
XX The invention relates to a transgenic plant cell (I) transformed by a
XX phosphatase stress-related protein (PHSRP) coding nucleic acid
XX (ABR81330-ABR81334), where expression of the nucleic acid in the plant
XX cell results in increased tolerance to an environmental stress as
XX compared to a wild type variety of the plant cell. PHSRP encoding genes
XX are useful for identifying Physcomitrella patens and related organisms,
XX as markers for specific regions of the genome, mapping of genomes of
XX organisms related to P. patens, identification and localisation of P.
XX patens sequences of interest, evolutionary studies, determination of
XX PHSRP regions required for function, modulation of a PHSRP activity,
XX modulation of the metabolism of one or more cell functions, modulation
XX of the transmembrane transport of one or more compounds and modulation
XX of stress resistance. The gene is also useful for identifying and/or
XX cloning PHSRP homologues in other cell types and organisms, for
XX identifying an organism as being P. patens or its close relative and for
XX evolutionary and protein structural studies. The present sequence is that
XX of a PHSRP of the invention.
XX Sequence 353 AA;

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PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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Alignment Scores:

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PR	09-AUG-1999;	9905-0147493;
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PR	10-AUG-1999;	9905-0148171;
PR	11-AUG-1999;	9905-0148319;
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PR	13-AUG-1999;	9905-0148684;
PR	16-AUG-1999;	9905-0149368;
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PR	18-AUG-1999;	9905-0149426;
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PR	20-AUG-1999;	9905-0149723;
PR	20-AUG-1999;	9905-0149929;
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PR	23-AUG-1999;	9905-0149930;

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PR	28-OCT-1999	99US-0161921
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Alignment Scores:	
Pred. No.:	1.45e-28
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DB:	21
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Matches:	112
Conservative:	59
Mismatches:	32
Indels:	13
Gaps:	13

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Db 58 ThirsteralalysMetMetValAspThr-----SerAlaGly 69
Oy 351 GAAGCAAGAAGATGCGACAGTGAAGACCTTGTGGAAAGAACTTTGTAAAGCCTTCGTG 410
      ||||| :|||
Db 70 GlulysArgGlieSerLeuValAspMetProProGluIlyValAlaAspArgGlyGlyTyrIle 89
Oy 411 ATCTTGGCTCTGAAG-----GGCTATGTGCTGAGCGGAG 446

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Dd	90	GLYGLYGLYTRPLeuAsnAspArgSerLeuSerCysGlyTyrCysSerPheArg----	108
Qy	447	GGTGAAGGAGAGAAATGACAGATGCGCCAGATGTCATCTGGAAACATCAACCGAGAGTGT	506
Dd	109	GLYAsnArgSerThrMetGlnAspPheArgLeuLeuValSerThrIleGlyGly----	127
Qy	507	AGGCGCCCATCGTCCCTCATTACTCGGGGTTCATATTTGCTGTTTGAATGGACATGGA	566
Dd	128	-----GlnAlaValCysMetPheGlyIlePheArgGlyIleGly	140
Qy	567	GGAAATTCAGCCTCAAAATTTGCTGCACAGACAGATTTGGCATCAAACTTATACAGAAATTT	626
Dd	141	GLYSerArgAlaIleGlyTyrLeuValGlnHisIlePheAsnAlaMetMet-----LysHis	159
Qy	627	CCTTAAGAGATGATGATCACTGATAGAAAACCTGAAGAGATGCGCTTTTGGACATTTTC	686
Dd	160	ProGln-----PheLeuThrAspThrLeuValAlaLeuAsnGlnThrTyr	174
Qy	687	AAGCATATCTGATGAAGATGTTCTCTTAACAGATCTCCAGCAGAAACGCTGGCTGAAGAA--	743
Dd	175	LYSGlnThrAspValAlaPheLeuGlu-----SerGlnLysArgThrTyrAspArg	191
Qy	744	GATGGGTCACATCGCCAGCTGGTGTCTGCTGGTACCAACATCTTTATTTGGCAACATTC	803
Dd	192	AspGlySerThrAlaSerAlaValIleValIleGlyAsnHisIleuTyrValAlaAsnVal	211
Qy	804	GGAGATATGTCGGGCAATCTTGCTGTCGTTAATAGAGAGATCAAAACATGACGCTTA	863
Dd	212	GLYAspSerArgThrIleVal-----SerLysAlaGlyLysAlaIle	225
Qy	864	AGCCTAGCGAAAGACATATATTCGATCTCACTAGATGAAAGCGGATGAGATATCAAGAGCT	923
Dd	226	AlaLeuSerAspPheLeuArgTyrAsnArgSerAspGlnArgLysValGlyIleGluSerAla	245
Qy	924	GGAGGAACGTCAGG-----GATGGCGCTGTTTGGCGCTGTCAGAGGTGCACGC	974
Dd	246	GLYGLYValIleMetThrAlaGlyIleThrTTPArgValGlyGlyValIleLeuAlaMetSerArg	265
Qy	975	TCCATTTGGGAGCGGACAGTACAGACGCGTCGAGTGTCACTCTGTGCCCGACATCAGACGC	1034
Dd	266	AlaPheGlyAsnArgMetLeuLysGlnPhe--ValValAlaGlnProGlnIleGlnAsp	284
Qy	1035	TGCACAGTCACCCCCCAATGACAGAGGTTCAATTGTTGGCTGGTGAATGGCTCTTCAAGATC	1094
Dd	285	LeuGlnIleAspHisGlyAlaGlyIleLeuValIleLeuAlaSerAspGlyLeuThrAspVal	304
Qy	1095	TTTATCCCAAGAAAGACCGGTAACTTCATCTTGTCTGCTGCAGAGATGAAGAAAGATCCAG	1154
Dd	305	ValProAsnGluAspAlaVal-----AlaLeuAlaGlnSerGluGlnGluPro-----	320
Qy	1155	ACCCGGGAGGGAGATCGCGACGCGACGCGCTACGAAAGACAGCCTGCACAGACGTCGCGC	1214
Dd	321	-----GlnAlaIleAlaIleArgLysLeuThr	328
Qy	1215	AACAGAGCGGTGCACGCGGGCTCGCGCCGACAACTGCATCTGTGAATGCTGGTGGCGAGATGGG	1274
Dd	329	AspThrAlaPheSerArgGlySerThrIleAspAsnIleThrCysIleValValLysPheArg	348
Qy	1275	CAC	1277
Dd	349	His	349
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AC	ABB08398;		
XX			
XX	16-MAY-2002	(first entry)	
DE		Human-derived protein phosphatase.	

Human: protein phosphatase; calmodulin-dependent phosphoenzyme II;
phosphorylation.

OS Homo sapiens.
XX XX
XX JP2001333776-A.
XX PD
XX 04-DEC-2001.
XX PF
XX 25-MAY-2000; 2000JP-0154223.
XX PR
XX 25-MAY-2000; 2000JP-0154223.
XX PA
XX (DOKU-) DOKURITSU GYOSEI HOJIN SANGYO GIJUTSU SO.
XX PA (SUNKR) SUNTORY LTD.
XX WP1; 2002-135942/18.
XX DR N-PSDB; ABA97280.
XX XX
XX A human-derived protein phosphatase and its inhibitor -
XX XX
XX Claim 1; Page 8-9; 15pp; Japanese.
XX PS
XX
XX The invention relates to a human-derived protein phosphatase which has
CC protein phosphatase activity, in which the dephosphorylating amino acid
CC is threonine-specific, which requires Mg^{2+} for the dephosphorylating
CC reaction. The therapeutic agent of the invention can be used for the
CC diseases caused by inactivation of calmodulin-dependent phosphoenzyme II.
CC The current sequence represents a human-derived protein phosphatase.
XX XX
XX Sequence 454 AA;
SQ

Alignment Scores:
Pred. NO.: 1.51e-28 Length: 454
Score: 366.50 Matches: 127
Percent Similarity: 42.86% Conservative: 65
Best Local Similarity: 28.35% Mismatches: 145
Query Match: 14.32% Indels: 111
DB: Gaps: 16

US-09-935-124A-1 (1-1422) x ABB08398 (1-454)
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QY 183 CTTCTTGAAGACCTCCCTCCGCGCAGCAGTACTGACTAGAGATCAGGAGGAGACCTTTGCTT 242
DB 26 LeuLeuGlnAspPheProAlaLeuLeuAsnProGlu----- 37
QY 243 TTGGAGAGATCTCCGACCGGAGAGGCGGAT-----TCAGGT 281
DB 38 ---AspProLeuProTprLysAlaProGlyThrValLeuSerGlnGluValGluGly 56
QY 282 TCTCTTGGCC----- 290
DB 57 GlnLeuAlaGlnLeuAlaMetGlyPheLeuGlySerAlaGlyAlaProProProLeuAla 76
QY 291 -----ACATCAATTCGCGAGTCGTAAGACTGA-----GGG 323
DB 77 AlAlaLeuAlaHisGlnValValSerGlnLeuLeuGlnThrAspLeuSerGluPheArg 96
QY 324 AAGAGCGCAAGAGAAAACCTCCGAGAGAGAGACAGATCGACTGAAGCTTTGGCA 383
DB 97 LysLeuProArgGlnGluGlnGluGlnGlnGlnAspAspArgGluGluValAlaPro 116
QY 384 AAGAAAGTTTGAAGACCTCTTCGATGATCTTTGGTGTGAAGGGCTATGGCGTACGGG 443
DB 117 ValThrLeuLeuAspAlaGlnSerLeuValaGlnSerPheAsnArgLeuTTPGluVal 136
QY 444 AAGGGTGAG----- 452
DB 137 AlGlyGlnTrrGlnValGlnValProLeuAlaAlaArgAlaSerGlnArgGlnTrrLeu 156

QY 453 -----AGGAGAGATCGAGATGCCACGTCATCTG 485
DB 157 ValSerIleH1a1a1eArgenThrArgGlyMetGlnbprgh1sValSerLeu 176
QY 486 AAGACATCAGCAGAGAGGTAGGCCCCCATCTGCTCATTAATCTGGGTTTCATTTT 545
DB 177 ProSerPhe--AsnGlnLeuPheGlyLeuSerAspProValAsnArg--AlaTyPhe 194
QY 546 GCTGTTTGTATGACATGAGAGATTGCGACCTCAAAATTGCTGTCACAGAAATTGCAT 605
DB 195 AlaValPheAspGlyH1sGlyValAlaPheAlaAlaArgTyAlaAlaValH1sValH1s 214
QY 606 CAAAATTATACAGAAA-----TTTCTAAAGAGATGTAATCACTGTA 650
DB 215 ThrAsnAlaAlaArgGlnProGlnLeuProThrAspProGlnGly----- 229
QY 651 GAGAAAAACCGTGAAGATGCCCTTTGGACACTTTCAGCATCTCATGAAAGTTCTT 710
DB 230 -----AlaLeuArgGlnAlaPheArgArgThrAspGlnMetPheLeu 243
QY 711 AAACAAGCTTCAGCAGAGACCTGCTGGAAAAGATGGGTCCTGCAAGTGTCTTG 770
DB 244 ArgLybAlbLysArgGlnArg-----LeuGlnSerGlyThrThrGlyValCysAlaLeu 261
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DB 262 IleAlaGlyAlaThrLeuH1sValAlaTrpLeuGlyAspSerGlnValIleLeuVal---- 280
QY 831 TTATATGAGAGAGATCAAAAACATGACGCTTAAGCTTCAGCAAAAGATTAATCTCACT 890
DB 281 -----GlnIleGlnValValLybLeuMetGlnProH1sArgProGln 295
QY 891 CAGTATGAAGCCGATGAGATACAGAGCTGAGAAAACGTCAGGGAT----- 941
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QY 942 GGGCGCTTTTGGCGCTGTAGAGGTGTCACGCTCCATTGGGACCGGACGTAACAAGCC 1001
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DB 335 ProTyValSerGlyGlybAlaAspAlaAlaSerArgAlaLeuThrGlySerGlnbprTy 354
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QY 1122 ATCTGTCTGTCTCGAGATGAAAAGATCAGACCCGGGAAAGGAAGTCCGACGCCGAC 1181
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QY 1182 GCGCCGCTAGAGAGACCTGCAACAGGCTGGCCACAGCGCGGTGAGGGGCTCGGCC 1241
DB 389 ValAlaGlnGly-----LeuValAlaAlaAlaArgGlnArgGlySerH1s 403
QY 1242 GACAAGCTCATGTATGGTGGG 1265
DB 404 AspAsnIleThrValMetValVal 411

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DT 17-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 19292.
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KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
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PR	28-OCT-1999	99US-0161922
PR	29-OCT-1999	99US-0161933
PR	29-OCT-1999	99US-0162142

Alignment Scores:

Pred. No.:	2.4e-28
Score:	364.00

Percent Similarity: 48.13%
Best Local Similarity: 32.56%

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Query Match: 14.228
DB: 21
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US-09-935-124A-1 (1-1422) X AAG18041 (1-358)

249 GATCTCCACCCCGTAGCAGTGGCGATTGAGTTCTCTTGGCACAATCATATATCCAGATG 308

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Db      15 AspmetProGluLysValAspAspGlyGlyTyrile----- 27
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309 GTAAGACTGAAGGGAAGGCAAAAGAAAACTCCGAGGAGAGAAGATGGCAGT 368

Db 28 -----GIYGIYGIYTrpLys-----AsnAspAspGlySer 37

369 GAGAGCTTGTGAAAAGAACTTTGTAAAGCCTTCGCGATCTTTGGTCTGAAGGC 428

Db 38 leuSer-----Cys-----Gly 41

429 TATGTGCTGAGCCGAGGGTGAGAGGAGAGATCCAGATGCCCATCTCATCTGAAC 488

Db 42 TyrCysSerPheArg---GlyLysArgSerThrMetGluAspPheTyrAspIleLysAla 60

489 GACATCACCGAGAGTGTAGGCCCCCAATGTCCTATTACTCGGTTTCATATTTGCT 548

Db 61 SerThrIleGluGly-----GlnAlaValAlcysMetPheGly 72
Qy 549 GTTTTGTGATGACATGAGAAATTGAGCCTCAAAATTTGTCGACAGATTTCATCAA 608
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 73 ILePheArgGlyHisGlyIleSerAlaGluIleuLysGluHisLeuPheArg 92
609 AACCTTAATCAGAAATTTCTTAAGAGAGATGTAATCATGCTGAGAGAAACCTGAAGAGA 668
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 93 AenLeuMet---LysHisProGln-----PheLeuThrArgThrLysLeu 106
Qy 669 TGGCTTTTGGACATCTTCAACGACTACTGATGAAGACTCTTAAACACTCTCCAGCCGAG 728
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 107 AlaLeuAenGlnThrLysGlnThrAspValAlaPheLeuGln-----SerGln 123
Qy 729 AAGCTGCTGTGAAA---GATGGGTCACTGTCGACCTGTGTTCTGCTGTAGCAACATT 785
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Db 124 LysAspThrTyrArgAspArgGlySerThrAlaSerAlaValLeuValGlyAenHis 143
Qy 786 CTTTATATATGCTCAACCTCGAGATAGTACGGGCACATCTTGCTGCTTATATAGAGAGCT 845
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Db 281 IleValValLysPheArgHis 287
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AC AAG39776;
DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
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XX AAG18040;
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XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EPI033405-A2.
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US-09-935-124A-1 (1-1422) x AAG18040 (1-359)

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Search completed: February 9, 2003, 17:54:43
Job time : 87 secs

GenCore version 5.1.3
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OM nucleic - protein search, using frame_plus.n2p model

Run on: February 9, 2003, 17:55:34 ; Search time 15.5 Seconds
(without alignments) 4067.708 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 50 summaries

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9: /cg21_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp:*
10: /cg21_6/ptodata/2/pubpaa/US09_PUBCOMB.pcp:*
11: /cg21_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp:*
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13: /cg21_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp:*
14: /cg21_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2018	78.8	392	9	US-09-935-124A-2
2	395.5	15.4	274	10	US-09-860-351-4
3	375.5	14.7	353	10	US-09-828-302-14
4	358.5	14.0	361	9	US-10-178-977A-2

5	358.5	14.0	361	9	US-10-178-977A-4	Sequence 4, Appl1
6	358.5	14.0	361	9	US-10-178-977A-6	Sequence 6, Appl1
7	338	13.2	382	10	US-09-972-741-2	Sequence 2, Appl1
8	319	12.5	390	10	US-10-072-130-3	Sequence 3, Appl1
9	317.5	12.4	281	10	US-09-801-368-278	Sequence 278, App
10	317	12.4	372	9	US-09-973-961-4	Sequence 4, Appl1
11	317	12.4	372	10	US-09-973-965-4	Sequence 4, Appl1
12	317	12.4	372	10	US-09-973-064-4	Sequence 4, Appl1
13	317	12.4	372	10	US-09-973-071-4	Sequence 4, Appl1
14	317	12.4	372	10	US-09-973-063-4	Sequence 4, Appl1
15	317	12.4	372	10	US-09-973-964-4	Sequence 4, Appl1
16	317	12.4	372	10	US-09-975-964-4	Sequence 4, Appl1
17	317	12.4	372	10	US-09-975-072-4	Sequence 4, Appl1
18	317	12.4	372	10	US-09-972-038-4	Sequence 4, Appl1
19	317	12.4	372	10	US-09-972-757-4	Sequence 4, Appl1
20	313	12.2	478	9	US-09-973-965-4	Sequence 4, Appl1
21	313	12.2	478	9	US-10-072-130-1	Sequence 1, Appl1
22	312	12.2	373	10	US-09-925-300-1655	Sequence 1655, Ap
23	312	12.2	400	10	US-09-925-300-1254	Sequence 1254, Ap
24	297.5	11.6	387	10	US-09-866-987-9	Sequence 9, Appl1
25	283	11.1	352	10	US-09-860-351-2	Sequence 2, Appl1
26	276	10.8	371	10	US-09-828-302-15	Sequence 15, Appl1
27	265.5	10.4	491	9	US-10-114-893-69	Sequence 69, Appl1
28	242.5	9.5	228	10	US-09-900-715-2	Sequence 2, Appl1
29	206	8.0	459	10	US-09-866-987-8	Sequence 8, Appl1
30	191	7.5	149	10	US-09-860-351-6	Sequence 6, Appl1
31	185.5	7.2	2026	10	US-09-801-368-86	Sequence 86, Appl1
32	178	7.0	504	9	US-10-158-895-2	Sequence 2, Appl1
33	178	7.0	504	12	US-10-123-427-2	Sequence 2, Appl1
34	178	7.0	513	9	US-10-158-895-43	Sequence 43, Appl1
35	178	7.0	517	9	US-10-158-895-11	Sequence 11, Appl1
36	154	6.0	504	12	US-09-860-351-5	Sequence 5, Appl1
37	153.5	6.0	114	10	US-09-752-820A-2	Sequence 2, Appl1
38	153.5	6.0	282	10	US-09-813-310A-2	Sequence 2, Appl1
39	153.5	6.0	143	10	US-09-866-987-10	Sequence 10, Appl1
40	128.5	5.0	143	10	US-09-866-987-10	Sequence 10, Appl1
41	116	4.5	549	9	US-09-902-325-42	Sequence 42, Appl1
42	114	4.5	293	9	US-09-712-363-154	Sequence 154, Appl1
43	114	4.5	380	10	US-09-823-240-10	Sequence 10, Appl1
44	111	4.3	514	9	US-09-712-363-154	Sequence 154, Appl1
45	111	4.3	1163	10	US-09-893-348-1195	Sequence 1195, Ap
46	110	4.3	380	10	US-09-764-864-1195	Sequence 193, App
47	108.5	4.2	475	10	US-09-854-133-193	Sequence 193, App
48	108.5	4.2	786	10	US-09-738-973-193	Sequence 12663, A
49	107.5	4.2	786	10	US-09-815-245-12663	Sequence 8, Appl1
50	106.5	4.2	578	12	US-10-074-527-8	

ALIGNMENTS

RESULT 1
US-09-935-124A-2
Sequence 2, Appl1
Patent No. US20020156003A1
GENERAL INFORMATION:
APPLICANT: Lorens, James
APPLICANT: Xu, Weiduan
APPLICANT: Bogenberger, Jakob
FILE REFERENCE: 021044-000210us
CURRENT APPLICATION NUMBER: US/09/935,124A
PRIOR FILING DATE: 2002-05-21
PRIORITY APPLICATION NUMBER: 60/284,760
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens
US-09-935-124A-2

Alignment Scores:

Pred. No.: 2,616-170 Length: 392
 Score: 2018.00 Matches: 392
 Percent Similarity: 100.00% Conservative: 0
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 Query Match: 78.83% Indels: 0
 DB: 9 Gaps: 0

US-09-935-124A-1 (1-1422) x US-09-935-124A-2 (1-392)

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OY 222 GGATCAGGGGGACCTTGTGCTTTTGTGATGATCTCCACCCGCTAGCAGTGGCATTCAGT 281
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OY 282 TCTCTTGGCCACATCAATATCCAGATGTAAGCTGAAGGGAGGAGCAAGAGAGAA 341
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DB 61 SerLeuAlaThrSerIleSerGlnMetValLysThrGlnGlyLysGlyAlaLysArgLys 80
OY 342 ACCTCCGAGAGAGAGAGAGATGGCAGTGAAGACTTGTGAAAAGAAAGATTGTAAGCC 401
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DB 81 ThrSerGlnGlnGlnLysAenGlySerGlnLysGlnLysValGlnLysLysValCysLysAla 100
OY 402 TTTTGGGTGATCTTTGGTCTGAAGGGCTATGTGGCTGACCGGAGGGGTGAGAGGAGAG 461
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DB 101 SerSerValIlePheGlyLeuLysGlyLysValAlaGlnArgLysGlyLysArgGlnGln 120
OY 462 ATGCAGGATGCCACGTCATCTCGAAGCAGCATCCGAGAGGTAGGGCCCATCTGCTCC 521
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DB 141 LeuIleThrArgValSerThrPheAlaValPheAepGlyHisGlyGlyLysIleArgAlaSer 160
OY 582 AAATTTGGCTGCACAGAAATTTGCATCAAACTTAATCAGAAAATTTCTTAAGAGAGATGTA 641
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OY 642 ATCAGGTGAGAGAAACCGTAGAGATGCTTTTGGACACTTCAAGCATCTGATGTA 701
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OY 702 GAGTTCCTTAAACAAGCTTCCAGCCAGAGCTGCTGGAAGATGGTCCATGCGCAGC 761
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OY 762 TGTGTTCTGGCTGTGACAACTTTCTTAATATGCAACTTCGAGAGATGTGCGGCAATC 821
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OY 942 GGGCGTGTGTTGGCGGTGTAGAGGTGTACGCTTCATTTGGGAGCGGCGCATCAACGCG 1001
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RESULT 2

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US-09-860-351-4
; Sequence 4, Application US/09860351
; Patent No. US20020077463A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 38155-20013.00
; CURRENT APPLICATION NUMBER: US/09/860,351
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,260
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Consensus amino acid
US-09-860-351-4

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Alignment Scores:

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Percent Similarity: 395.50	Matches: 106
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DB: 10	Indels: 55
	Gaps: 13

US-09-935-124A-1 (1-1422) x US-09-860-351-4 (1-274)

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DB 21 LysAepSerTrp-----SerPhePheAlaValPheAepGlyHisGlyGlySer 36
OY 573 CGAGCTCAAAATTTGCTGCACAGAAATTTGCATCAAACTTAATC-----AGAAA 623
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DB 37 GlnAlaAlaLysTrpAlaGlyLysHisLeuHisLysThrIleLeuAlaGlnArgLysSer 56
OY 624 TTTCCCTAAGAGAT-----GTAACTAGTGAAGAAACCGTAGAAGAG 668
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DB 57 PheProGlnGlnLysAepProTrpGlnMetLysSerAepLeuGlnAepAlaLeuLysGly 76
OY 669 TGCCTTTGACACTTTTCAAGCATCTGATGAAGATTCTTAAACAAGCTTCAGC--- 725
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DB 77 SerPheLeuGlnAla-----AepThrAepGlnGlnLeuAenArgSerAlaGlnAlaSerAla 94
OY 726 -----CAGAACCTGCTCGAAGAGATGGGTCACTGCCACGTGTGTTCTG 770
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Db 266 SerAlaGluAsePProMetGluAlaAla 274

RESULT 3
US-09-828-302-14
; Sequence 14, Application US/09828302
; Patent No. US20020152502A1
; GENERAL INFORMATION
; APPLICANT: COSTA E SILVA, OSWALDO DA
; APPLICANT: VAN THIELEN, NOCHIA
; APPLICANT: CHEN, ROUYING
; APPLICANT: ISHITANI, MANABU
; TITLE OF INVENTION: IN PLANTS
; TITLE OF INVENTION: PHOSPHATASE STRESS-RELATED PROTEINS AND METHODS OF USE
; FILE REFERENCE: 16313-0029
; CURRENT APPLICATION NUMBER: US/09/828,302
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-302-14

Alignment Scores:
Pred. No.: 3,56e-25 Length: 353
Score: 375,50 Matches: 109
Percent Similarity: 43,78% Conservative: 60
Best Local Similarity: 28,24% Mismatches: 98
Query Match: 14,67% Indels: 119
DB: 10 Gaps: 12

US-09-935-124a-1 (1-1422) x US-09-828-302-14 (1-353)
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Db 20 ---AlaGluAsePArgLysIleu-----SerAlaMetGlnGlyTrpArgAsp 34
Qy 459 GAGATGACAGATGCCCCCGTCATCCCGAAGCAATCCAGCCGAGAGTATGAGCCCCCATCG 518
Db 35 SerMetGluAsePArgLysIleuAsePValIleuAsePValIleuAsePValIleuAsePVal 49
Qy 519 TCCCTCATTAATCGAGTTTCATATTTTGGCTTTTGTATGAGCATGAGAGTATGAGAGC 578
Db 50 -----ThrSerThrSerIlePheGlyIlePheAsePArgLysIleuYsLeuVal 66
Qy 579 TCAAAATTTGCTGCAAGAAATTTGATCAAAACTTAATCAGAAA-----TTTCTTAA 632
Db 67 AlaYsPheCysAlaYsHsIleuHsIleuGluValLeuYsSergIleuAlaYsAlaYs 86
Qy 633 GAGATGTATATCAGTGTAGAGAAAACCGTGAAGAGATGCTTTTGGACACTTTCAGACAT 692
Db 87 GlyAseP-----LeuYsAlaSerLeuGluYrSerPheLeuArg 99
Qy 693 ACTGATGAA-----GAGTTCTTAAACAGCT 719
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Qy 720 TCCAGGCA----- 728
Db 120 SerSerIleuAsePlyLeuGlyAseGlyAseGlyAseSerSerAsePAlaArgIleAsePAsp 139
Qy 728 ----- 728
Db 140 GluSerAsePTrpSerYrAlaValLeuThrlGluSerAsePAspSerAsePLeuAlaThrIlys 159
Qy 729 AAGCTGCTCGAAGAAAT-----GGTCACTGCGCACCTGTGTCTG 770
Db 160 LysHsIleYsYrSerAsePArgGlyProIleYrGlySerThrAlaValAlaLeu 179
Qy 771 GCTGTAGACAACTTTCTTTATTTGCAACCTCGAGATAGTCGGCAATCTTGTCGT 830
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Qy 831 TATATGAGAGAGTCAAAAACATGACGCTTAAGCTCAGCAAAAGCATATATCAACT 890
Db 200 ArgGlyGlu-----AlaValAsePLeuSerIleAsePHisYsPserAsn 213
Qy 891 CAGTATGAAGAGCGGATGAGATACAGAAAGCTGAGAGAAAGTCAAGGATGGCGTGT 950
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Qy 951 TTGGCGCTGTAGAGGTGACGCTCCCTTGGGAGCGGCAAGTACAG----- 998
Db 234 AseGlySerLeuAsePLeuThrlArgAlaIleGlyAsePMetGluPheGlyArgProAseP 253
Qy 999 -----CGTGCAGGTGTCACTCTGTGCGGACATCAGAGCGTGCACAGTGAAC 1046
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Qy 1107 GAAGCGGTGAATTCATCTTGTCTGTCTGATGAGATGAAGAATCCAGACCCGGAAGGG 1166
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Qy 1167 AAGTCCGAGCGACGCCCGCTACAGAGCAGCTGCAACAGGCTGGCCCAAGAGCGGTG 1226
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Qy 1227 -----CAGCGGGGCTCGGCGGACGACCAAGCTCATCTGTGATGTGTGTGCGGATA 1271

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Db 322 SerProthThrArgInglIngluGlyCybApsAmMetSerIleIleValGlnPro 341
Qy 1272 GGGCACTGAGGGGTGGCG 1289
Db 342 LysGlnSerGlyValAla 347

RESULT 4
US-10-178-977A-2
; Sequence 2, Application US/10178977A
; Publication No. US20030014776A1
; GENERAL INFORMATION:
; APPLICANT: University of Zurich
; APPLICANT: Cold Spring Harbor Laboratory
; APPLICANT: Grossniklaus, Ueli
; APPLICANT: Huck, No. US20030014776A1bert
; APPLICANT: Moore, James M.
; TITLE OF INVENTION: MATERNAL EFFECT GAMETOPHYTE REGULATORY POLYNUCLEOTIDE
; FILE REFERENCE: feironia
; CURRENT APPLICATION NUMBER: US/10/178,977A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/300,624
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-178-977A-2

Alignment Scores:
Pred. No.: 1,14e-23 Length: 361
Score: 358.50 Matches: 86
Percent Similarity: 51.25% Conservative: 58
Best Local Similarity: 30.60% Mismatches: 96
Query Match: 14.00% Indels: 41
Gaps: 8

US-09-935-124a-1 (1-1422) x US-10-178-977A-2 (1-361)
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Qy 504 TGTAGGCCCCCATCGTCCCTCATTTACTCGGGTTTCATATTTCGCTTTTGTAGGACAT 563
Db 99 IleGlySerSerThrGly-----AlaPheTyGlyValPheAspGlyHis 113
Qy 564 GGAGGAATTCGAGCTCAAAATTTGCTGCACAGAAATTCGATCAAAATTTATC----- 617
Db 114 GlyGlyValAAspAlaSerPheThrLysAsnIleMetLysLeuValMetGluAps 133
Qy 618 AAAAAATTTCTTAAGGAGATGTAATCACTGTAGAGAAACCGTGAAGATGCCCTTTTG 677
Db 134 LysHisPhePro-----ThSerThrLysLysAlaThrArg 145
Qy 678 GACACTTTCAAGCATCTGATGAGAGATTCTTAAACAAGCTTCCAGCAGAGCTGGCC 737
Db 146 SerAlaPheValLysThrAspHisAlaLeuAlaAAspAlaSerSerLeuApsArg----- 163
Qy 738 TGGAAAGATGGGTCCACTGCCACGTGTGTTTGGCTGTAGACAACTTTATATATGGC 797
Db 164 ---SerSerGlyThrThrLysLeuThrAlaLeuIleLeuApsLysThrMetLeuIleAla 182
Qy 798 AACCTCGGAGATAGTCGGGCAATCTTGTCGTATTAATGAGAGAGTGAAAAACATGCA 857
Db 183 AsnAlaGlyAAspSerArgAlaValLeu-----GlyLysArgGlyArg 196
Qy 858 GCCTTAAGCGCTGACAAAGACATTAATCAACTATGATGAGAGATGAGATGAG 917
Db 197 AlaIleGlnLeuSerLysAspHisLysProApsCysThrSerGlnArgLeuArgIleGlu 216
Qy 918 AAGCTGAGGAAACGTCAGGAGATGGCGGTGTTTGGCGTGTAGAGGTGTCAAGCTCC 977

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Db 217 LysLeuGlyGlyValIleTyAspGlyTyLysLeuApsGlnLysSerValAlaArgAla 236
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Qy 1023 GACATCAAGCGCTGCCACTGACCCCAATGACAGGTTTCATTTGTTGGCTGTAGTGG 1082
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Qy 1143 GAAAGATTCACAGCCCGGAGAGGAGATCCGACGCCGCGCTACGAGACAGCAGCTGC 1202
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Qy 1203 AACAGCTTGGCCCAACAGCGGCTGACGCGGCTGCGCCGACCAACTGATGTAGTGG 1262
Db 307 -----LeuValLysGluAlaLeuGlnArgAsnSerCysApsAsnLeuThrValVal 324
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Db 325 Val 325

RESULT 5
US-10-178-977A-4
; Sequence 4, Application US/10178977A
; Publication No. US20030014776A1
; GENERAL INFORMATION:
; APPLICANT: University of Zurich
; APPLICANT: Cold Spring Harbor Laboratory
; APPLICANT: Grossniklaus, Ueli
; APPLICANT: Huck, No. US20030014776A1bert
; APPLICANT: Moore, James M.
; TITLE OF INVENTION: MATERNAL EFFECT GAMETOPHYTE REGULATORY POLYNUCLEOTIDE
; FILE REFERENCE: feironia
; CURRENT APPLICATION NUMBER: US/10/178,977A
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/300,624
; PRIOR FILING DATE: 2001-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-178-977A-4

Alignment Scores:
Pred. No.: 1,14e-23 Length: 361
Score: 358.50 Matches: 86
Percent Similarity: 51.25% Conservative: 58
Best Local Similarity: 30.60% Mismatches: 96
Query Match: 14.00% Indels: 41
Gaps: 8

US-09-935-124a-1 (1-1422) x US-10-178-977A-4 (1-361)
Qy 444 AAGGGTGAAGGAGAGATGAGATGCGCATCTGTAAGCATCAACCGAGAG 503
Db 79 LysGlyProLysGlnSerMetGlnApsGlnPheIleCysValAAspAspLeuThrGluTy 98
Qy 504 TGTAGGCCCCCATCGTCCCTCATTTACTCGGGTTTCATATTTCGCTTTTGTAGGACAT 563
Db 99 IleGlySerSerThrGly-----AlaPheTyGlyValPheAspGlyHis 113
Qy 564 GGAGGAATTCGAGCTCAAAATTTGCTGCACAGAAATTCGATCAAAATTTATC----- 617
Db 114 GlyGlyValAAspAlaSerPheThrLysAsnIleMetLysLeuValMetGluAps 133

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[illegible]

Pred. No.:	1,146-23	Length:	361
Score:	358.50	Matches:	86
Percent Similarity:	51.25%	Conservative:	58
Best Local Similarity:	30.60%	Mismatches:	96
Query Match:	14,00%	Indels:	41
DB:	9	Gaps:	8

US-09-935-124A-1 (1-1422) x US-10-178-977A-6 (1-361)

QY	444	AAGGTTGAGAGGAGAGATGCAAGATGCCAGATGCCAGTCACTCTGAAGACATCACCGAGGAG	503
DB	79	LYSGLYPCTOLYSGINSERETGLUAPGLUHEHLECYVALASPRASEUTHGILUYR	98
QY	504	TGTAGGCCCCCATCGTCCCTCATTACTCGGGTTTCATATATTTGCTGTTTTGATGCACT	563
DB	99	ILEGLYSEETERTHGLY-----ALAEHYEGLYVALPHEASPGLYHLS	113
QY	564	GGAGAAATTCAGAGCTCAAAATTTGCTGCACAGAAATTTGCATCAAAACTTAATC-----	617
DB	114	GLYGLYVALAPRALAALASERPHETHIRLYSASNLLEWELCYEVALWELGULAP	133
QY	618	AGAAATTTTCCAAAGAGATGTAACTAGGTGATAGAGAAACCGTGAAGATGCGCTTTTG	677
DB	134	LYHNLAPHEP-----THSERTHIRLYSVALATIRARY	145
QY	678	GACACTTTCAAGCATACGTATGTAAGAGTTCTTAAACAACCTTCACGACAGAACTGCC	737
DB	146	SERLAPHEVALYRTHIRAPHLAALAEULASPRLASERSEIRLEUAPRAG-----	163
QY	738	TGCAAAAGATGGGTCCACCTGCCACGTGTGTTCGCTGTATGACAAACATTTTAAATATGCC	797
DB	164	-----SERSECTYRTHIRALALEUTHIRALAEULILEUAPRYRTHIRWELIUALA	182
QY	798	AACCTGGAGATATGTCGGGCAATCTTGTTGGTTATATGAGAGAGTCAAAACATGCA	857
DB	183	ASMLAPHEVALPSETHIRAGLAVALLEU-----GLYSEARGGLYARG	196
QY	858	GCTTAAACCTTACGAAAGAGACATAATCCAACTCAGTATGAAGAGGATGAGATACAG	917
DB	197	ALALIEULIUSERLYASPHSLYSPFOASNCYRTHIRGLIARGLEUNRGLIEGLU	216
QY	918	AAGCTGAGAGAAACGTACGAGATGGCGCTGTTTGGCGCTGTCAGAGATGACGCTCC	977
DB	217	LYSEULIYGLYVALILETYRAMPGLYTRYLEUANDGLYGLINEUSERVALAARGALA	236
QY	978	ATTGGGAGCGGCGACATACAG-----CGCTGCGGTGCACCTCTGTGCC	1022
DB	237	LEULIYASPRTHIRHILELYSGLYRTHIRLYSGLYSERLEUCYSPROUSEURCYSEGLUPRO	256
QY	1023	GACATACGAGCGCTGCACGTACGCCCAATGACAGGTTCAATTTTGTGGCTGTGATGCG	1082
DB	257	GLIULDELGLIULILEVALLEUTHIRGLIUGLUMAPGLIURYLEULILEWELGYCASPGLY	276
QY	1083	CTCTTCAAGGTCTTTTACCCGACGAAGAGCCGTGAATTCAATCTTGTCTGTCTGAGGAT	1142
DB	277	LEUTHIRAPRALWESERSEGLNCYSALEVALATHMETVAL-----ARGARG	292
QY	1143	GAAGAATTCAGACCGGGGAAGGAGAAATCGCACAGCCGCTGCTACGAAGCAGCTGC	1202
DB	293	GLIULDELTHIRHISAPRARGPROGLIARGCYSESEGINALA-----	306
QY	1203	AACAGCGTGGCCAAAGAGCGGTGCACGCGGCGTGGCGGCGCAACGTCACTGTGATGTG	1262
DB	307	-----LEUVALYSELULALEUGLIRHARGASERCYASAPAEULIUTHIRVALIVALI	324
QY	1263	GTG 1265	
DB	325	VAL 325	

RESULT 7
US-09-972-741-2
; Sequence 2, Application US/09972741
; Patent No. US20020100070A1

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; GENERAL INFORMATION:
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING
; FILE REFERENCE: R-723-CIP
; CURRENT APPLICATION NUMBER: US/09/972,741
; PRIOR FILING DATE: 2001-10-08
; PRIOR APPLICATION NUMBER: US 09/815,935
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,235
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/216,249
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-972-741-2

Alignment Scores:
Pred. No.: 7 596-22 Length: 382
Score: 338.00 Matches: 99
Percent Similarity: 48.67% Conservative: 47
Best Local Similarity: 33.00% Mismatches: 106
Query Match: 13.20% Indels: 48
DB: 10 Gaps: 11

US-09-935-124a-1 (1-1422) x US-09-972-741-2 (1-382)
Qy 417 GGCTGGAAGCGGTATGTGCTGAGCGAAGGCTGAGAGGAGATGCGAGATGCCACG 476
Db 21 Gtyleuargtlysermetglnlytrparygvalgluwtetglumbrplahls 40
Qy 477 GTCATCCTTAAGACGACATCCAGAGAGTGTAGGCCCCCATCTCTCTCACTTACGCGGTT 536
Db 41 ThrAlaValIleGlyLeu-----ProserGlyLeuGluThr--Trp 53
Qy 537 TCATATTTTGTGTTGTTGATGAGATGAGGAATTCGAGCCTCAAAATTTGCTGCACAG 596
Db 54 SerPhePheValValyLysPheGlyPheValGlySerGlnValAlaLysTyrcysGlu 73
Qy 597 AATTGTCATCAAACTTAATCAGAAATTTCTT-----AAAGAGATGTAATCACT 647
Db 74 HleleuLeuAspHisIleThrAsnAsnGlnAspPheArgGlySerIleGlyAlaProser 93
Qy 648 GTAGAGAAAACCGTAGAGATGCTTTTGACACTTTCAAGCATACTGATGAAGGTTTC 707
Db 94 ValGlu--AsnValLysAsnGlyIleArgThrGlyPheLeuGluIleAspGluHisMet 112
Qy 708 CTTAAACAAGCTTCCAGCCAGAACCTGCGTAAGATGGGTCACCTCCACGTTGT 767
Db 113 ArgValMetSerGlyLysHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
Qy 768 CTGGCTGTAGACAACATCTTTATATTATGCGCAACTCGAGATAGTGGGCAATCTGTGT 827
Db 133 LeuIleSerProGlnHisThrIyrPheIleAsnCyGlyAspSerArgGlyLeuLeuCyS 152
Qy 828 CGTTATATAGAGAGAGTCAAAAACATGACGCTTAAGCCTTAAGCCTCAAGAGACATAATCA 887
Db 153 Arg-----AsnArgLysValHisPhePheThrGlnAspHisLysPro 166
Qy 888 ACTCAGATATAGAGCGGATGAGATACAGAGAGCTGAGAGAACTCAGGATGGGCTT 947
Db 167 SerAsnProLeuGlnGlySerValArgIleGlnAsnAlaGlyLysSerValMetIleGlnArg 186
Qy 948 GTTTTGGCGCTGCTAGAGGTGTCAAGCTCATTTGGGAGCGGAGATGACAGGCTGC-- 1004
Db 187 ValaLenglySerLeuAlaValSerArgAlaLeuGlyAspPheAspItyLys--CysVal 205
Qy 1005 -----GTTGTCAAC-----TCTGTGCCGACATCAGA 1031
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Db 206 HisGlyLysGlyProThrGluGlnLeuValSerProGluValHisAspIleGlu 225
Qy 1032 CGCTCCAGACTGACCCCAATGACAGTTTCAATTTGTTGGCTGTGATGGCTTTCAAG 1091
Db 226 ArgSerGlu-----GluAspAspGlnPheIleIleLeuAlaCyAspGlyIleTrpAsp 243
Qy 1092 GTCTTACCCAGAAAGACCGGTGAACTTCATCTTGTCTGTCTGAG-----GATGA 1145
Db 244 ValMetGlyAsnGluGlnLeuCyAspPheValArgSerArgLeuGluValThrAspAsp 263
Qy 1146 AAGATCCAGACCCGGGAGAGGAAAGTCCGACCGCCGCTAGAGACAGCCTGCAAC 1205
Db 264 -----LeuGluLysValCyAsn 269
Qy 1206 AGCTGCGCAACAAAGCGGTGACGCGGCTCGCGGACCAAGTCACTGTATGTGTG 1265
Db 270 GluValAlaAspThrCysLeuTyrltyrGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 8
US-10-072-130-3
; Sequence 3, Application US/10072130
; Patent No. US20020173022A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Goli, Surya K.
; Lal, Preeti
; Corley, Neil C.
; Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/072,130
; FILING DATE: 05-Feb-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-4166
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1247927
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-072-130-3

Alignment Scores:
Pred. No.: 3 666-20 Length: 390
Score: 319.00 Matches: 96
Percent Similarity: 44.95% Conservative: 51
Best Local Similarity: 29.36% Mismatches: 124
Query Match: 12.46% Indels: 56
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Db 140 GlnArgLysLeuThrAlaAsnValGlyAspSerArgIleValLeuPheArgAsnGly 159
QY 837 GAGGAGAGTCAAAAACATCAGCCTTAAGCCTTCAGCAAGACATATCAATCTCAGTAT 896
Db 160 Aaa-----SerIleArgLeuThrTyrAspHisLysAlaSerAspThr 173
QY 897 GAAGACCGGATGATGATACAGAAAGCTTGAGAGAAACGTACAGGATGGCGTTTGGGC 956
Db 174 LeuGluMetGlnArgValGluGlnAlaGlyLeuIleMetLysSerArgValAsnGly 193
QY 957 GAGTACAGGTGTCACCGCTCCAGTGGGACGGGACGTACAGGCGCTGCGGTGACCTCT 1016
Db 194 MetLeuAlaValThrArgSerLeuGlyAspLysPhePheAspSerLeuValAlaGlySer 213
QY 1017 GTGCCGACATCAGACGCTGCCAGCTGACCCCAATGACAGGTTCAATTTGTGGCCTGT 1076
Db 214 ---ProPheThrThrSerValGluIleThrSerGluAspLysPheLeuIleLeuAlaCys 232
QY 1077 GATGGGCTCTTCAAGTCTTTTACCAGCAAGAACGCGTGAATCTCATCTTGTCTGTCTC 1136
Db 233 AspGlyLeuThrAspValIleAspAspGlnAspAlaCysGluLeuIleLysAspIleThr 252
QY 1117 GAGGATGAAAGAATCCAGACCCGGGAAGGAATGCCGACCCGCGCTACAGAGA 1196
Db 253 GluProAsnGlu----- 256
QY 1197 GCCTGCACAGCGCTGGCCCAAGCGGCTGCAGCGGCGCTCGCCGCAACGTCACTGTG 1256
Db 257 AlaAlaLysValLeuValArgTyrAlaLeuGluAsnGlyThrThrAspAsnValThrVal 276
QY 1257 ATGGTGGTG 1265
Db 277 MetValVal 279
RESULT 10
US-09-973-941-4
Sequence 4, Application US/09973941
Patent No. US2002016465A1
GENERAL INFORMATION:
APPLICANT: Roche, Jean-Marc
APPLICANT: Roche, Jean-Marc
APPLICANT: Heichman, Karen
TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
TITLE OF INVENTION: Diseases
FILE REFERENCE: Protein Interactions in ND
CURRENT APPLICATION NUMBER: US/09/973,941
CURRENT FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: US 60/240,790
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: US 60/304,775
PRIOR FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 372
TYPE: PRT
ORGANISM: Homo sapiens
US-09-973-941-4
Alignment Scores:
Fried. No.: 5.38e-20 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.33% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Gaps: 114
DB: 9 Gaps: 15
US-09-935-124A-1 (1-1422) x US-09-973-941-4 (1-372)
QY 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGAGATGATGATCA----- 221
Db 27 LeuLeuGlnAspAspArgArgValThrProThrCysHisSerSerThrSerGluProArg 46

QY 222 -----GGATCAGGGGACCTTTGTTTGATGAT----- 251
Db 47 CysSerArgPheAspProAspGlySerGlySerProLathrTrpAspAsnHeGlyLe 66
QY 252 -----CTCCACCCCGCTAGACAGTGGCATTCAGGT 281
Db 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
QY 282 TCTTGGCCACATCAATATCCAGATGGTAAAGACTGAAGGGAAGAGCAAAAGAGAAAA 341
Db 81 ----- 81
QY 342 ACCTCCGAGAGAGAGAAATGCGAGTGAAGACTTTGGAAGAAAGTTGTAAAGCC 401
Db 82 -----LysTyrGly-----LysProIleProLysIle 90
QY 402 TCTTGGGATGATTTTGTGTGAAGGCTATGTGCTGAGCCGGAAGGATGAGAGAGAG 461
Db 91 SerLeuGluAsnValGlyCysAlaSerGlnIleGlyLysArgLys--GluAsnGluAsp 109
QY 462 ATGCAGATGCCACGTCATCCTGMAACGACATCACCGAGAGTGAAGGCCCATGCTCC 521
Db 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
QY 522 CTGATTAAGTCCGGTTTCATATTTGCTGTTTGAATGACATGAGAAATTCAGACCTCA 581
Db 120 -----ValLeuTyrPheAlaValIleThrAspGlnHisGlyGlyProAlaAlaIle 135
QY 582 AAATTGCTGCACAGAAATTTGATCAAAATTTAATCAAGAAATTTCTTAAAGAGATGA 641
Db 136 AspPheCysHisThrHisMetGlnLysCysIleMetAspLeuLeuProLys----- 152
QY 642 ATCAGTGTAGAGAAAACCGTAAGAGATGCTTTTGGACACTTTTCAACATATCTAGTAA 701
Db 153 -----GluLysAsnLeuGlnThrLeuLeuThrLeuAlaPheLeuGlnLysAsp 169
QY 702 GAGTTCCTTAAACAGCT-----TCAGCCAGAAAGCTGCGTGAAGATGGTCCACT 755
Db 170 AlaPheSerSerHisAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 189
QY 756 GCCAGGTGTGTTGGCTGTGACAACTTT--CTTTATTTGCCAACCTGGAGATAGT 812
Db 190 AlaThrValAlaLeuLeuArgAspGlyIleGluLeuValAlaAlaSerValGlyAspSer 209
QY 813 CGGGCAATCTTGTGTCGTTATATGAGAGAGTCAAAACATGACGCTTAAAGCTTCAGC 872
Db 210 ArgAlaIleLeuCysArg-----LysGlyLysProMetLysLeuThr 223
QY 873 AAAGACATTAATCCAACTCAGTATGAGAGCGGATGAGATACAGAAAGCTGAGAGA--- 929
Db 224 IleAspHisThrProGluArgLysAspGlnLysGlnIleLysLysCysGlyGlyPhe 243
QY 930 -----AACGTACAGGATGGCGCTGTTTGGCGCTTGAAGAGTGCAGCTCC 977
Db 244 ValAlaThrAsnSerLeuGlyGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 263
QY 978 ATTGGGACCGGACGTACAGCGGCTGCGTCACTTGTGCGGACATGACAGCTGCG 1037
Db 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGlnThrLysArgIle 283
QY 1038 CAGCTG--ACCCCAATGACAGGTTCAATTTGTGGCTGATGGCTCTTCAAGGTC 1094
Db 284 LysLeuHisHisAlaAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
QY 1095 TTTTACCCCAAGAAAGGCGGTGAATCTTCACTTGTGCTGTCTGCAGAGATGAAAGATCCAG 1154
Db 304 ValAsnSerGlnGluIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
QY 1155 ACCCGGGAAGGAAGTCCGACGCGACCGCGCTACGAAAGACGCTGCAAGCGCTGCGC 1214
Db 322 -----AlaAlaHisAlaValThr 327
QY 1215 AACAAAGCGGTGACGCGGCGCTCGCCGACAAAGCTGATGATGTTGTTGCGATAGGG 1274


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; ORGANISM: Homo sapiens
US-09-973-064-4

Alignment Scores:
Pred. No.: 5,386-20      Length: 372
Score: 317.00           Matches: 112
Percent Similarity: 41.32%      Conservative: 57
Best Local Similarity: 27.38%    Mismatches: 126
Query Match: 12.38%           Indels: 114
DB: 10                      Gaps: 15

US-09-935-124A-1 (1-1422) x US-09-973-064-4 (1-372)

OY 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGACACTGACTCA----- 221
    |||||  |||||
DB 27 LeuLeuGlnAspAspArgValThrProThrCysHisSerSerThrSergIuProArg 46
OY 222 -----GATCAGGGGACCTTTGCTTTTATGAT----- 251
    |||||  |||||
DB 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTTPAspAspPheGlyIle 66
OY 252 -----CTCCACCCGCTAGACAGTGCGGATTCAGGT 281
    |||||  |||||
DB 67 TTPAspAspArgIleAspGluProIleLeuLeuProProSerIle----- 81
OY 282 TCTCTTCCACATCAATATCCAGATGTAAGACTGAAGAGGAAAGACAAAGAAAA 341
    |||||  |||||
DB 81 ----- 81
OY 342 AACTCCGAGAAAGAGAAATGGCACTGTAAGACTTTGTAAAGCC 401
    |||||  |||||
DB 82 -----LysPyrGly-----LysProIleProIle 90
OY 402 TCTTCGGTATCTTTGGTGAAGGGCTATGTGGCTAGCGGAGGGTGAAGAGAGAG 461
    |||||  |||||
DB 91 SerLeuGlnAspValGlyCysAlaSerGlnIleGlyLysArgLys---GlnSerGlnAsp 109
OY 462 ATGCAAGATGCCACGTCATCTGTAAGCAATCAGCAAGAGAGTGAAGCCCATGTC 521
    |||||  |||||
DB 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
OY 522 CTCATTACTCGGGTTTCATATTTTGTCTTTTGTATGACATGAGAGAAATGAGCTTA 581
    |||||  |||||
DB 120 -----ValLeuLysPheAlaValItyAspGlyHisGlyGlyProAlaAlaAla 135
OY 582 AAATTGTGTCACAGAAATTGTCACAACTTAATCAGAAAAATTTCTAAGAGATGTA 641
    |||||  |||||
DB 136 AspPheCysHisThrHisMetGlnLysCysIleMetAspLeuProLys----- 152
OY 642 ATCAGTGTAGAGAAAACCGTGAAGAGATGCTTTTGGACACTTTCAGACATGATGAA 701
    |||||  |||||
DB 153 -----GlnLysAsnLeuGluThrLeuLeuThrLeuAlaPheLeuGluIleAspLys 169
OY 702 GAGTTCTTAAACAGCT-----TCCAGCCAGAACCTGCTGGAAGATGGGTCACCT 755
    |||||  |||||
DB 170 AlaPheSerSerHisIleAlaArgLeuSerAlaAspAlaThrLeuLeuThrSergIyThrThr 189
OY 756 GGCAGGTGTGTTGGCTGTAGACAACTT-----CTTATATGGCCAACTCCGAGATAT 812
    |||||  |||||
DB 190 AlaThrValAlaLeuLeuArgAspGlyIleGlnLeuValValAlaSerValGlyAspSer 209
OY 813 CGGGCAATCTTGTGTCGTTATATATGAGAGAGTCAAAAAATGCAAGCTTAAAGCTCAGC 872
    |||||  |||||
DB 210 ArgAlaIleLeuCysArg-----LysGlyLysProMetCysLeuThr 223
OY 873 AAAGACATATTCACACTAGATGAAGCGGATGAGATACAGAAAGCTGAGAGA--- 929
    |||||  |||||
DB 224 IleAspHisThrProGlnArgLysAspGlnLysGlnArgIleLysLysCysGlyGlyPhe 243
OY 930 -----ACGTCAGGATGGCGCTTTTGGGGGTGCTAGAGGTTCACGCTCC 977
    |||||  |||||
DB 244 ValAlaTTPAspAspSerLeuGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 263

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OY 978 ATTGGGAGACGGGACAGTACAAAGCGCTGCGGTGTCACTCTGTGCCCCGACATCAGACGCTGC 1037
    |||||  |||||
DB 264 IleGlyAspLeuAspLeuThrSergIyValIleAlaGluProGluThrArgIle 283
OY 1038 CAGCTG---ACCCCAATGACAGGTTTCAATTTTGGCTGGCTGATGGGCTTTCAGATC 1094
    |||||  |||||
DB 284 LysLeuHisHisAlaAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
OY 1095 TTTACCCCAAGAAAGACCGGTGACCTTCTGCTCTGTCGAGAGATGAAGAAATCCAG 1154
    |||||  |||||
DB 304 ValAsnSerGlnGlnIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
OY 1155 ACCCGGAGAGGAGACTCCGACGCCGACGCCCTGACGAAGACCTGCACAGCTGACC 1214
    |||||  |||||
DB 322 -----AlaAlaHisAlaValThr 327
OY 1215 AACAAAGCGGTGACAGGGGCTCGGCCCAACAGTCTGTGATGTGTGTGGATAGGG 1274
    |||||  |||||
DB 328 GlnGlnAlaIleGlnTyrGlyThrGlnAspAsnSerThrAlaValAlaProPheGly 347
OY 1275 CACTGAGGGGTGCGCGCGGCCAGGAG 1301
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DB 348 AlaTTPGlyLysTyrLysAsnSergIu 356

RESULT 13
US-09-973-077-4
; Sequence 4, Application US/09973077
; Patent No. US20020114799A1
; GENERAL INFORMATION:
; APPLICANT: Koch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US/09/973,077
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-077-4

Alignment Scores:
Pred. No.: 5,386-20      Length: 372
Score: 317.00           Matches: 112
Percent Similarity: 41.32%      Conservative: 57
Best Local Similarity: 27.38%    Mismatches: 126
Query Match: 12.38%           Indels: 114
DB: 10                      Gaps: 15

US-09-935-124A-1 (1-1422) x US-09-973-077-4 (1-372)

OY 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGACACTGACTCA----- 221
    |||||  |||||
DB 27 LeuLeuGlnAspAspArgValThrProThrCysHisSerSerThrSergIuProArg 46
OY 222 -----GATCAGGGGACCTTTGCTTTTATGAT----- 251
    |||||  |||||
DB 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTTPAspAspPheGlyIle 66
OY 252 -----CTCCACCCGCTAGACAGTGCGGATTCAGGT 281
    |||||  |||||
DB 67 TTPAspAspArgIleAspGluProIleLeuLeuProProSerIle----- 81
OY 282 TCTCTTCCACATCAATATCCAGATGTAAGACTGAAGAGAAAGACAAAGAAAA 341
    |||||  |||||
DB 81 ----- 81

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OY 342 ACCGCCGAGAGAGAGAAATGCGATGAGAGCTTGTGAAAAAAGTTTGTAAAGCC 401
    |||
    |||
    |||
Db 82 -----LysTyrGly-----LysProIleProIle 90
    |||
    |||
    |||
OY 402 TCTTCGGTATCTTTGGTCTGAAGGCTATGTGCTGAGCGGAAGGTTGAGGAGAG 461
    |||
    |||
    |||
Db 91 SerLeuGluAnValGlyCybAlaSerGlnIleGlyLysArgLys---GluAnGluAsp 109
    |||
    |||
    |||
OY 462 ATGCAGATGAGCCATCTGATCTGAAGCATCATCCGAGAGAGTTAGGCCCATCTGTC 521
    |||
    |||
    |||
Db 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
    |||
    |||
    |||
OY 522 CTCATTACTCGGGTTTCATATTTTGTGTTTGTATGACATGAGAGATTGAGCTCA 581
    |||
    |||
    |||
Db 120 -----ValLeuTyrPheAlaValTyrAspGlnIleGlyLysProIleAlaIle 135
    |||
    |||
    |||
OY 582 AAATTTGCTGCACAGAAATTTGCATCAAACTATACAGAAATTTCTTAAAGAGATGA 641
    |||
    |||
    |||
Db 136 AspPheCybHleThrIleMetGluLysCysIleMetAspLeuLeuProLys----- 152
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OY 642 ATCAGTTAGAGAAAACCGTGAAGATGCTTTTGGACATTTCAAGCATACTGATGA 701
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Db 153 -----GluLysAsnLeuGlnThrLeuMetThrLeuAlaPheLeuGluIleAspLys 169
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OY 702 GAGTTCTTAAACAAGCT-----TCCAGCCAGAAAGCTGCCGTGAAGATGGGTCAT 755
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Db 170 AlaPheSerSerHisAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 189
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OY 756 GCCACGTGTGTTCTGGCTGTAGACACATTT---CTTTATATTTGCCAATCTCGAGATAGT 812
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Db 190 AlAThrValAlaLeuLeuAlaArgAspGlyIleGlnLeuValValAlaSerValGlyAspSer 209
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OY 813 CGGGCAATCTTGTGCTGTTATATAGAGAGAGTCAAAAACATGACAGCTCAAGCTCAAG 872
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Db 210 ArgAlaIleLeuCybArg-----LysGlyLysProMetLysLeuThr 223
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OY 873 AAAGAGATATATCAACTCAAGTAAAGAGCGAGATATCAAGAAAGCTGAGAGA--- 929
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Db 224 IleAspHisThrProGlnArgLysAspGlnLysGlnArgIleLysLysCybGlyGlyPhe 243
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OY 930 -----ACGTCAGGAGATGGGCGTGTGTTGGGCGTCTGAGAGTCTCAAGCTCC 977
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Db 244 ValAlaIlePheAsnSerLeuGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 263
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OY 978 ATTGGGAGCGGCGATGACAGCGCTGGGCTGACCTCTGTCGCCGAGCATGACAGCGCTGC 1037
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Db 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGlnProIleThrLysArgIle 283
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OY 1038 CAGCTG---ACCCCAATGACAGTTCAATTTTGTGCGCTGATGGGCTCTTCAAGTTC 1094
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Db 284 LysLeuHisHisAlaAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
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OY 1095 TTATACCCAGAGAAAGCCCTGAATCTTCTGCTGTCGAGATGAAAAAGATCCAG 1154
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Db 304 ValAsnSerGlnIleLeuCybAspPheValAsnGlnCybHisAspProAsnGlu----- 321
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OY 1155 ACCCGGAGAGAGAAATGCCAGACCGCCGCTACAGACAGACCTGCAAGAGCTGAGC 1214
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Db 322 -----AlaAlaHisIleAlaValThr 327
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OY 1215 AACAAAGCGGTGAGCGGGCTCGGCCAGAACCTCACTGTATGTGTGTGCGGATAGGG 1274
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Db 328 GluGlnAlaIleGlnIlyrGlyThrGluAspSerThrAlaValAlaProPheGly 347
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OY 1275 CACTGAGGCGGTGCGCGCGCCAGGAG 1301
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Db 348 AlaTyrPheLysTyrLysAsnSerGlu 356
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RESULT 14
 US-09-973-063-4
 ; Sequence 4, Application US/09973063
 ; Patent No. US20020115119A1
 ; GENERAL INFORMATION:

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; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,063
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-063-4

Alignment Scores:
Pred. No.: 5.38e-20 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.32% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Indels: 114
Gaps: 15

US-09-935-124A-1 (1-1422) x US-09-973-063-4 (1-372)
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OY 222 -----GATCAGGGGACCTTCTCTTTGTATGAT----- 251
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Db 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTyrAspAsnPheGlyIle 66
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OY 252 -----CTCCACCCGCTACAGAGTGGGATTCAGGT 281
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Db 67 TyrAspAsnArgIleAspGlnProIleLeuLeuProProSerIle----- 81
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OY 282 TCTCTGCCACATCAATATCCAGATGTGAAGACTGAAGAGAAAGAGCAAAAA 341
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Db 81 ----- 81
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OY 342 ACCGCCGAGAGAGAGAAATGCGATGAGAGCTTGTGAAAAAAGTTTGTAAAGCC 401
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Db 82 -----LysTyrGly-----LysProIleProIle 90
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OY 402 TCTTCGGTATCTTTGGTCTGAAGGCTATGTGCTGAGCGGAAGGTTGAGGAGAG 461
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Db 91 SerLeuGluAnValGlyCybAlaSerGlnIleGlyLysArgLys---GluAnGluAsp 109
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OY 462 ATGCAGATGAGCCATCTGATCTGAAGCATCATCCGAGAGAGTTAGGCCCATCTGTC 521
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Db 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
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OY 522 CTCATTACTCGGGTTTCATATTTTGTGTTTGTATGACATGAGAGATTGAGCTCA 581
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Db 120 -----ValLeuTyrPheAlaValTyrAspGlnIleGlyLysProIleAlaIle 135
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OY 582 AAATTTGCTGCACAGAAATTTGCATCAAACTATATCAAGAAATTTCTTAAAGAGATGA 641
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Db 136 AspPheCybHleThrIleMetGluLysCysIleMetAspLeuLeuProLys----- 152
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    |||
OY 642 ATCAGTTAGAGAAAACCGTGAAGATGCTTTTGGACATTTCAAGCATACTGATGA 701
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    |||
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Db 153 -----GluLysAsnLeuGlnThrLeuMetThrLeuAlaPheLeuGluIleAspLys 169
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OY 702 GAGTTCTTAAACAAGCT-----TCCAGCCAGAAAGCTGCCGTGAAGATGGGTCAT 755
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Db 170 AlaPheSerSerHisAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 189
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OY 756 GCCACGTGTGTTCTGGCTGTAGACACATTT---CTTTATATTTGCCAATCTCGAGATAGT 812
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Db      190 ALATHTValAlaLeuLeuArgAspGlyIleGluLeuValAlaLaserValGlyAspSer 209
QY      CGGGCAATCTTGTGCTGTTATATAGAGAGATCAAAACATGCACCCCTTAAGCCCTCAG 872
Db      210 ArgAlaIleLeuCyArg-----LysGlyLysProMetLysLeuThr 223
QY      873 AAGAGCATTAATCCAACTCAGATGAGAAGCCGATGAGATACAGAAGCCTGAGAGA--- 929
Db      224 IleAspHisThrProGluThrGlySerGluGlyIleGlyValGlySerGlyGlyPhe 243
QY      930 -----AAGCTCAGGATGGCGGTGTTGGCGGTGCTAAGGTGTCAAGCTCC 977
Db      244 ValAlaTrpAsnSerLeuGlyGlnProHisValAsnGlyArgLeuLamethrArgSer 263
QY      978 ATTGGGAGCGGAGATGACAGCGCTGCGGTGCTGCTGTCGCGACATCAGAGCCTGC 1037
Db      264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGluThrLysArgIle 283
QY      1038 CAGCTG---ACCCCAATGACAGGTTCAATTTGTTGGCGCTGTGATGGGCTTTCAAGCTC 1094
Db      284 LysLeuHisIleValAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
QY      1095 TTTAACCCCAAGAAAGCCGTGAATCTTCTGCTGCTCGAGGATGAAAAGATCCAG 1154
Db      304 ValAsnSerGlnGluIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
QY      1155 ACCCGGAAAGGAAAGTCCGACCGACCGCCGCTACGAAGCAGCTGCAGAGCTGCC 1214
Db      322 -----AlaAlaHisAlaValThr 327
QY      1215 AACAAAGCGGTGACGAGCGGCTCGCCGACAAAGCTCAGTGTGATGTTGGTGGAGATGGG 1274
Db      328 GluGlnAlaIleGlnThrGlyThrGluAspAsnSerThrAlaValValValProPheGly 347
QY      1275 CACTGAAGGGGTGGCGCGCCGACGAGG 1301
Db      348 AlaTrpGlyLysTrpLysAsnSerGlu 356

RESULT 15
US-09-973-964-4
; Sequence 4, Application US/09973964
; Patent No. US20020115606A1
; GENERAL INFORMATION:
; APPLICANT: Roche, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,964
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-964-4

Alignment Scores:
Pred. No.: 5,38e-20 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.33% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Indels: 114
DB: 10 Gaps: 15
US-09-935-124a-1 (1-1422) x US-09-973-964-4 (1-372)

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QY      180 CTGCTTTTGTATGAC-----CTCCCTCCGGCCAGCACTGACTCA----- 221
Db      27 LeuLeuGlnAspAspArgArgValThrProThrCysHisSerSerThrSerLysProArg 46
QY      222 -----GGATCAGGGGACCTTTGCTTTTGTATGAT----- 251
Db      47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTrpAspAsnHeGlyIle 66
QY      252 -----CTCCACCCCGCTAGACAGGGGCAATTCAGGT 281
Db      67 TrpAspAsnArgIleAspGluProIleLeuLeuProPheSerIle----- 81
QY      282 TCTCTTGGCCATCAATATGCCAGATGTGAAGAAGCTGAAGGAAAGCAAAAGAAAA 341
Db      81 ----- 81
QY      342 ACCTCCGAGAAAGAAAGAAATGGCAGTGAAGACTTTGGAAAAGAAAGTTTGAAGCC 401
Db      82 -----LysTrpGly-----LysProIleProLysIle 90
QY      402 TCTTGGGATCTTTGTTGTTGATGAGGCTATGCGCTGAGCGGAGGTGAGAGGAGAG 461
Db      91 SerLeuGluAsnValGlyCysAlaSerGlnIleGlyLysArgLys-----GluAsnGlnAsp 109
QY      462 ATGCAGATGCCCAAGCTATCCTGAACGACATCAACCGAGAGTGAAGCCCATCTGTC 521
Db      110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
QY      522 CTCATTAATCCGGGTTTCATATTTTCTGTTTGTATGACATGACAGAAATTCAGACCTCA 581
Db      120 -----ValLeuLysPheAlaValGlyArgArgGlyHisGlyIleProAlaIleAla 135
QY      582 AAATTGCTGCACAGAAATTTGATCAAACTTAACAGAAATTTCTTAAGAGAGATGA 641
Db      136 AspPheCysHisThrHisMetGlnLysCysIleMetAspLeuLeuProLys----- 152
QY      642 ATCACTGTAGAAAACCGTGAAGAGATGCTTTTGAACATTTTCAGACATGATGA 701
Db      153 -----GluLysAsnLeuGlnThrLeuLeuThrLysAlaPheLeuGlnIleAspLys 169
QY      702 GAGTTCCTTAACAAGCT---TCCAGCCAGAAAGCTGCTGGAAGAAAGTGGTCACT 755
Db      170 AlaPheSerSerHisAlaArgLeuSerIleAspAlaThrLeuLeuThrSerGlyThrThr 189
QY      756 GCCAGGTGTGTTGCGGTGAGCAACAT---CTTTATTTGCCAAGCTGGAGATAGT 812
Db      190 AlaThrValAlaLeuLeuArgAspGlyIleGluLeuValAlaLaserValGlyAspSer 209
QY      813 CGGGCAATCTTGTGCTGTTATATAGAGAGATCAAAACATGCACCCCTTAAGCCTCAGC 872
Db      210 ArgAlaIleLeuCyArg-----LysGlyLysProMetLysLeuThr 223
QY      873 AAGAGCATTAATCCAACTCAGATGAGAAGCCGATGAGATACAGAAGCCTGAGAGA--- 929
Db      224 IleAspHisThrProGluThrGlySerGluGlyIleGlyValGlySerGlyGlyPhe 243
QY      930 -----AAGCTCAGGATGGCGGTGTTGGCGGTGCTAAGGTGTCAAGCTCC 977
Db      244 ValAlaTrpAsnSerLeuGlyGlnProHisValAsnGlyArgLeuLamethrArgSer 263
QY      978 ATTGGGAGCGGAGATGACAGCGCTGCGGTGCTGCTGTCGCGACATCAGAGCCTGC 1037
Db      264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGluThrLysArgIle 283
QY      1038 CAGCTG---ACCCCAATGACAGGTTCAATTTGTTGGCGCTGTGATGGGCTTTCAAGCTC 1094
Db      284 LysLeuHisIleValAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
QY      1095 TTTAACCCCAAGAAAGCCGTGAATCTTCTGCTGCTCGAGGATGAAAAGATCCAG 1154
Db      304 ValAsnSerGlnGluIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321

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OY 1155 ACCCGGAAGGAGTCCGCAAGCCCGCTACGAAGCACTTCGACAGGCTGGCC 1214
DB 322 -----AlaAlaHisAlaValThr 327
OY 1215 AACAAAGCGGTGACGAGCGGCTCGCGCAACAAGCTGATGTGATGGTGGATAGGG 1274
DB 328 GluGlnAlaIleGlnIrrGlyThrGluAspAsnSerThrAlaValValProPheGly 347
OY 1275 CACTGAGGGGTGGCGCGCGGACAGAG 1301
DB 348 AlaTrpGlyLysTrpLysAsnSerGlu 356

RESULT 16
US-09-975-072-4
; Sequence 4, Application US/09975072
; Patent No. US20020115607A1
; GENERAL INFORMATION:
; APPLICANT: Roche, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE OF INVENTION: Diseases
; CURRENT APPLICATION NUMBER: US/09/975,072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-072-4

Alignment Scores:
Pred. No.: 5,38e-20 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.32% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Indels: 114
DB: 10 Gaps: 15

US-09-935-124a-1 (1-1422) x US-09-975-072-4 (1-372)
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OY 222 -----GATCAAGGGGAGACCTTTCCTTTTGTATGAT----- 251
DB 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTTPAspAsnPheGlyIle 66
OY 252 -----CTCCACCGCGCTAGACAGTGGCGATTCAGGT 281
DB 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
OY 282 TCTCTTCCACATCAATATCCAGATGTTAAAGACTGAAGGAAAGACAAAGAGAAA 341
DB 81 ----- 81
OY 342 ACCTCGAGAGAAAGAGATGCGAGTGAAGACTTGTGAAAAGATTGTGAAGCC 401
DB 82 -----LysTrpGly-----LysProIleProLysIle 90
OY 402 TCTTCGGTATCTTTGGTCTTAAGAGGGCTATGCTGAGCGGAGAGGAGAGAGAGAG 461
DB 91 SerLeuGlnAsnValGlyCysAlaSerGlnIleGlyLysArgLys-----GluAsnGluAsp 109
OY 462 ATCGAGATGCCACGATCTCTTAAGACATACGAGAGATGTAGAGGCCCATCTCTCC 521
DB 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119

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DB 120 -----ValLeuTrpPheAlaValIrrAspGlyHisGlyValProAlaAlaIle 135
OY 582 AAATTTCGTCGACAGAAATTCATCAAAACTTAATCAAGAAAATTCCTTAAGAGATGA 641
DB 136 AspPheCysHisThrHisIleMetCulLysCysAlaIleAspLeuLeuProLys----- 152
OY 642 ATCAGTGTAGAGAAAACCGTGAAGAGATGCCCTTTTGGACACTTTCAGACATATGATGA 701
DB 153 -----GluLysAsnLeuGlnIrrThrLeuLeuThrLeuAlaPheLeuGlnIleAspLys 169
OY 702 GAGTTCCTTAACAGACT-----TCCAGCCAGAGAGCTGCTGGAAGAGATGGCTCACT 755
DB 170 AlaPheSerSerHisAlaArgLeuSerIleAspAlaThrLeuLeuThrSerGlyThrThr 189
OY 756 GCCACGTGTGTCTGCTGTGTAGACAACTT-----CTTATATTTGCCACCTCGAGATAGT 812
DB 190 AlaThrValAlaLeuLeuAspGlyIleGluLeuValValAlaSerValGlyAspSer 209
OY 813 CGGCAATCTTGTGTCTGTATATGAGAGAGTCAAAACATGACAGCCCTTAAGCTCAGC 872
DB 210 ArgAlaIleLeuGlyArg-----LysGlyLysProMetLysLeuThr 223
OY 873 AAAGAGCATATCAACTCAGTATGAGAGCGGATGAGTACAGAGAGCTGAGGA--- 929
DB 224 IleAspHisThrProGluLysArgAspGluLysGluLysGlyGlyPhe 243
OY 930 -----AACGTACAGGATGGCGGTGTTTGGCGCTGTAGAGGTCAAGCTCC 977
DB 244 ValAlaTrpAsnSerLeuGlnProHisAlaValAsnGlyArgLeuAlaMetThrAspSer 263
OY 978 ATTTGGGACCGGCGATACACAGCGCTGCGGTGTCACCTGTGTGCGCCGACATCAAGCTGC 1037
DB 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleLeuGlnProGluThrLysArgIle 283
OY 1038 CAGCTG---ACCCCAATGACAGGTTTCATTTTGTGCGCTGTATGAGGCTTCAGAGTTC 1094
DB 284 LysLeuHisHisAlaAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPheMet 303
OY 1095 TTAAACCCAGAGAGACCGCTGAATCTTCATCTTCCTGCTCGAGAGATGAATAAGATCCAG 1154
DB 304 ValAsnSerGlnGlnIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
OY 1155 ACCCGGAAGGAGTCCGCAAGCCCGCTACGAAGCAAGCTTCGACAGGCTGGCC 1214
DB 322 -----AlaAlaHisAlaValThr 327
OY 1215 AACAAAGCGGTGACGAGCGGCTCGCGCAACAAGCTGATGTGATGGTGGATAGGG 1274
DB 328 GluGlnAlaIleGlnIrrGlyThrGluAspAsnSerThrAlaValValProPheGly 347
OY 1275 CACTGAGGGGTGGCGCGCGGACAGAG 1301
DB 348 AlaTrpGlyLysTrpLysAsnSerGlu 356

RESULT 17
US-09-972-038-4
; Sequence 4, Application US/09972038
; Patent No. US20020119155A1
; GENERAL INFORMATION:
; APPLICANT: Roche, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE OF INVENTION: Diseases
; CURRENT APPLICATION NUMBER: US/09/972,038
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-038-4

Alignment Scores:
  Pred. No.:      5,38e-20      Length:      372
  Score:          317.00        Matches:     112
  Percent Similarity: 41.32%    Conservative: 57
  Best Local Similarity: 27.38%  Mismatches:  126
  Query Match:    12.38%       Indels:      114
  DB:             10           Gaps:         15

US-09-935-124A-1 (1-1422) x US-09-972-038-4 (1-372)

QY 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGCAGTACTGCTCA----- 221
DB 27 LeuLeuGlnAspAspArgValThrProThrCysHisSerSerThrSerGluProArg 46
QY 222 -----GGATCAGGGGGGACCTTTGCTTTTGATGAT----- 251
DB 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTrpAspAsnPhcGlyLe 66
QY 252 -----CTCCACCCGCTAGCAGTGGCCATTGAGT 281
DB 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
QY 282 TCTCTTGCCACATCATATCCCGATGTAAAGACTGAAGGAAAGGAAAGCAAGAAAA 341
DB 81 ----- 81
QY 342 ACCTCCGAGAAAGAGAATGGCAGTGAAGACTTGTGAAAAAGAAAGTTGTTAAAGCC 401
DB 82 -----LysTyrGly-----LysProIleProIle 90
QY 402 TCTTCGGTATCTTTGGTGTGAAGGCTATGTGGCTGAGCGGAAAGGCTGAGAGGAG 461
DB 91 SerLeuGlnAsnValGlyCysAlaSerGlnIleGlyLysArgGly--GluAsnGluAsp 109
QY 462 ATGCAGGATGCCACGTCATCCGAAAGCATCAGCAGGAGAGTGAAGGCCCATGCTCC 521
DB 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
QY 522 CTCATTACTCGGGTTTCATATTTTGTGTTTGTGATGACATGAGAAATTCGAGCCTCA 581
DB 120 -----ValLeuThrPheAlaValTyrAspGlyHisGlyCylProAlaAlaAla 135
QY 582 AAATTTGTCACACAGATTGCTCAAAATTATATCAAAAAATTCTTAAGAGAGATGA 641
DB 136 AspPheCysHisThrHisMetGluLysCysIleMetAspLeuLeuProLys----- 152
QY 642 ATCAGTGTAGAGAAACCGTGAAGAGATGCCTTTGGACACTTTCAGACTACTGTGA 701
DB 153 -----GluLysAsnLeuGluThrLeuLeuThrLeuAlaPheLeuGluIleAspLys 169
QY 702 GAGTTCCTTAAACAGCT-----TCCAGCCAGAAAGCTGCTGAAAGAGGTCCTCACT 755
DB 170 AlaPheSerSerHisIleAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 189
QY 756 GCCAGCTGTGTTGCTGCTGCTAGACAACATT--CTTTATATTGCCAAGCTCGAGATAGT 812
DB 190 AlaThrValAlaLeuLeuArgAspGlyIleGluLeuValAlaIleAspValGlyAspSer 209
QY 813 CGGGCAATTTGTGCTGTATATATGAGAGAGTCAAAACATGACAGCTTAAGCCCTACAC 872
DB 210 ArgAlaIleLeuCysArg-----LysGlyLysProIleLeuLeuThr 223
QY 873 AAAGACATATTCACACTAGTATGAGAGCGGATGAGAGCAGATCAGAAAGCTGAGAGA-- 929
DB 224 IleAspHisThrProGluArgLysAspGlyLysGluArgIleLysLysCysGlyGlyPhe 243
QY 930 -----AACGTCAGGAGTGGCGTGTGTTGGCGGTCTAGAGGTGTCAAGCTCC 977

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DB 244 ValAlaTrpAsnSerLeuGlyGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 263
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DB 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGluThrLysArgIle 283
QY 1038 CAGCTG---ACCCCAATGACAGTTTCATTTGTGGCTGTGATGGCTTTCAGAGTTC 1094
DB 284 LysLeuHisIleAlaAspAspSerPheLeuValLeuThrThrAspGlyIleAsnPhcMet 303
QY 1095 TTTACCCCAAGAAAGACCGTGAACCTTCATCTTGTCTGCTGAGAGATGAAAAAGTCCAG 1154
DB 304 ValAsnSerGlnGluIleCysAspPheValAsnGlnCysHisAspProAsnGlu----- 321
QY 1155 ACCCGGAAAGGAGTCCGACAGCCAGCCCGCTACGAAGACCTGCAGACAGCTGGCC 1214
DB 322 -----AlaAlaHisIleAlaValThr 327
QY 1215 AACAGCGCGTGCAGCGGGGCTCGCGCCGACACATGCTGATGTGATGGTGGCATAGCG 1274
DB 328 GluGlnAlaIleGlnTyrGlyThrGluAspAsnSerThrAlaValValProPheGly 347
QY 1275 CACTAGGGGGTGGCGCGCGCCAGAG 1301
DB 348 AlaTrpGlyLysTyrLysAsnSerGlu 356

RESULT 18
US-09-972-757-4
; Sequence 4, Application US/09972757
; Patent No. US2002011927A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,757
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-757-4

Alignment Scores:
  Pred. No.:      5,38e-20      Length:      372
  Score:          317.00        Matches:     112
  Percent Similarity: 41.32%    Conservative: 57
  Best Local Similarity: 27.38%  Mismatches:  126
  Query Match:    12.38%       Indels:      114
  DB:             10           Gaps:         15

US-09-935-124A-1 (1-1422) x US-09-972-757-4 (1-372)

QY 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGCAGTACTGCTCA----- 221
DB 27 LeuLeuGlnAspAspArgValThrProThrCysHisSerSerThrSerGluProArg 46
QY 222 -----GGATCAGGGGGGACCTTTGCTTTTGATGAT----- 251
DB 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTrpAspAsnPhcGlyLe 66
QY 252 -----CTCCACCCGCTAGCAGTGGCCATTGAGT 281
DB 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
QY 282 TCTCTTGCCACATCATATCCCGATGTAAAGACTGAAGGAAAGGAAAGCAAGAAAA 341

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Db 81 ----- 81
342 ACCTCGAGAGAGAAATGCGAGTGAAGACTTGTGAAAAGAAAGTTGTAAAGCC 401
82 -----LysTyrGly-----LysProIleProIle 90
402 TCTTCGGTATCTTGGCTGAAGGGCTATGTGGCTAGCGGAGGGTGAAGAGAGAG 461
91 SerLeuGluAenValGlyCysAlaSerGlnIleGlyLysArgLys---GluAenGluAer 109
462 ATGCGAGATGCCAGATCTCGAAGCATCGACGAGAGAGATGAGGCCCATGTC 521
110 ArgPheAerP-----PheAlaGlnLeuThrAerPoliu----- 119
522 CTCATTAATCTGGGTTTCAATTTTGTCTGTGATGACATGAGAGAAATTCGAGCTCA 581
120 -----ValLeuTyrPheAlaValIleTyrAerGlyIleGlyProAlaAlaIle 135
582 AAATTTGTCACAGAAATTCGATCAAAACTTAATGAGAAAATTTCTTAAAGAGATGA 641
136 AerPheCysAlaThrIleMetGluLysCysIleMetAerPheLeuProLys----- 152
642 ATCAGTGTAGAGAAAACCGTAGAGATGCTTTTGACACTTTCAGACATCTGATGA 701
153 -----GluLysAenLeuGlnThrLeuLeuThrLeuAlaPheLeuGluIleAerLys 169
702 GAGTTCCTTAAACAAGCT-----TCCAGCCAGAACCTGCTGAGAAAGTGGTCACT 755
170 AlaPheSerSerHisAlaArgLeuSerAlaAerAlaThrLeuLeuThrSerGlyThrThr 189
756 GCCACGTGTCTGCTGTGTAGACAACTT-----CTTATATATCCCACTCGAGATAGT 812
190 AlaThrValAlaLeuLeuAerAerGlyIleGluLeuValAlaSerValGlyAerSer 209
813 CGGCGCATCTTGTGTGTTATATGAGAGAGTCAAAAACATGACACCTTGAAGCTCAGC 872
210 ArgAlaIleLeuLysArg-----LysGlyLysProMetLysLeuThr 223
873 AAAGAGCATATCCAGTCAATGATGAGAGCGGATGAGATGACAGAGCTGAGAGA--- 929
224 IleAerHisThrProGluArgLysAerPoliuLysGluArgIleLysLysCysGlyPhe 243
930 -----AACGTGAGAGTGGGCTGTGTGTTGGGCTGTGAGTGGCTGACGCTCC 977
244 ValAlaThrAerSerLeuGlyLysProHisValAenGlyArgLeuAlaMetThrAerSer 263
978 ATTGGGAGCGGAGATGACAGCGCTGCGCTGTCACTGTGTGCCGACATCAAGCTGC 1037
264 IleGlyAerPheLysAerPheLysThrSerGlyValIleAlaGlnProGluThrAerGlyIle 283
1038 CAGCTG---ACCCCAATGACAGGTTCAATTTTGGCTGTGATGGCTCTTCAAGCTC 1094
284 LysLeuHisAlaAerPheAerPheLeuValLeuThrThrAerPheMet 303
1095 TTATCCCGAGAGAGCGGTGAATTCATCTTGTCTGTCTCGAGATGAAAAGATCCAG 1154
304 ValAerSerGlnGlnIleCysAerPheValAenGlnCysHisAerProAenIle----- 321
1155 ACCCGGAGAGGAGATCCGACGCGACCGCGCTACAGACAGCTGCAAGCGTGGCC 1214
322 -----AlaIleHisAlaValThr 327
1215 AACAGGCGGTGAGCGGGCTCGCGCCAGACGCTCACTGATGTGGTGGAGTAAAGG 1274
328 GluGlnAlaIleGlnIlyArgIlyThrGluAerAerSerThrAlaValValProPheGly 347
1275 CACTGAGGCTGCGCGCGCGCCAGAG 1301
348 AlaTyrPoliuLysTyrLysAenSerGlu 356

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RESULT 19
US-09-973-965-4

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; Sequence 4, Application US/09973965
; Patent No. US20020124273A1
; GENERAL INFORMATION:
; APPLICANT: Roche, Jean-Marc
; APPLICANT: Batteil, Paul L.
; APPLICANT: Hechtman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,965
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-973-965-4

Alignment Scores:
Pred. No.: 5,39e-20 Length: 372
Score: 317.00 Matches: 112
Percent Similarity: 41.32% Conservative: 57
Best Local Similarity: 27.38% Mismatches: 126
Query Match: 12.38% Indels: 114
Gaps: 15
DB: 15

US-09-935-124a-1 (1-1422) x US-09-973-965-4 (1-372)
QY 180 CTGCTCTTGAATGAC-----CTCCCTCCGCGCAGAGATCACTCA----- 221
DB 27 LeuLeuGlnAerPheArgValAlaThrProHisCysHisSerSerHisSerGluProArg 46
QY 222 -----GATCAGCGGAGACTTCTCTTGTGAAGAT----- 251
DB 47 CysSerArgPheAerProAerPoliuSerGlySerProAlaThrThrAerPheArgIle 66
QY 252 -----CTCCACCCGCTGACAGTGGGATTCAGT 261
DB 67 TrpAerAerArgIleAerPoliuProIleLeuLeuProProSerIle----- 81
QY 282 TCTCTCCACATCAATATCCAGATGGTAAAGACTGAAGGAGAAAGAGAGAAA 341
DB 81 ----- 81
QY 342 ACCTCGAGAGAGAAATGCGAGTGAAGACTTGTGAAAAGAAAGTTGTAAAGCC 401
DB 82 -----LysTyrGly-----LysProIleProIle 90
QY 402 TCTTCGGTATCTTGGCTGAAGGGCTATGTGGCTAGCGGAGGGTGAAGAGAGAG 461
DB 91 SerLeuGluAenValGlyCysAlaSerGlnIleGlyLysArgLys---GluAenGluAer 109
QY 462 ATGCGAGATGCCAGATCTCGAAGCATCGACGAGAGAGATGAGGCCCATGTC 521
DB 110 ArgPheAerP-----PheAlaGlnLeuThrAerPoliu----- 119
QY 522 CTCATTAATCTGGGTTTCAATTTTGTCTGTGATGACATGAGAGAAATTCGAGCTCA 581
DB 120 -----ValLeuTyrPheAlaValIleTyrAerGlyIleGlyProAlaAlaIle 135
QY 582 AAATTTGTCACAGAAATTCGATCAAAACTTAATGAGAAAATTTCTTAAAGAGATGA 641
DB 136 AerPheCysAlaThrIleMetGluLysCysIleMetAerPheLeuProLys----- 152
QY 642 ATCAGTGTAGAGAAAACCGTAGAGATGCTTTTGACACTTTCAGACATCTGATGA 701
DB 153 -----GluLysAenLeuGlnThrLeuLeuThrLeuAlaPheLeuGluIleAerLys 169
153 -----GluLysAenLeuGlnThrLeuLeuThrLeuAlaPheLeuGluIleAerLys 169

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OY 969 TCACGCTCCATTGGGGAACGGCAGTACAAAGCCGTCGGT----- 1007
DB 199 SerAgaLaLeuGlyAspTYrAspTYrLysCyValAspGlyLysGlyProThrGluGln 218
OY 1008 ---GTCACCTCTGTGCCGACATACAGCCTCCAGCTGACCCCAATGACAGTTTCAT 1064
DB 219 LeuValSerProGluProGluValTYrGluIleLeuAraGluGluGluAspGluPheIle 238
OY 1065 TTGTTGGCTGTGATGGGCTCTTCAGGCTTTTACCCAGAAAGACCCGTAACCTCATC 1124
DB 239 IleLeuAlaCyAspGlyIleTrpAspValMetSerAraGluGluIleuCySgluTYrVal 258
OY 1125 TTGCTCTGTCTGAGATGAAGAATCCAGACCCGGAAAGGAGTCCGACGCCAGCC 1184
DB 259 LysSerArgLeuGlu-----ValSerAsp 266
OY 1185 CGCTACGAGCAGCCTGCAACAGGCTGCGCAACAGCCGTCGACGGGGCTGCGCCGAC 1244
DB 267 AspLeuGluAsnValCyAsnTrpValValAspThrCySleuHisLysGlySerAAsp 286
OY 1245 AACGTCACGTGATGCTGTG 1265
DB 287 AsnMetSerIleValLeuVal 293

RESULT 21
US-10-072-130-4
Sequence 4, Application US/10072130
Patent No. US20020173022A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Golli, Surya K.
Lal, Preeti
Corley, Neil C.
Zhang, Hong
TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/072.130
FILING DATE: 05-Feb-2002
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US/08/873.093
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0319 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-4166
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1452526
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-072-130-4

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Alignment Scores:
Pred. No.: 1,36e-19 Length: 478
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
DB: 9 Gaps: 8

US-09-935-124a-1 (1-1422) x US-10-072-130-4 (1-478)
OY 333 AAGAGAAAACTCCAGAAAGAAAGAAATGCGACGTGAAGACCTTGTGAAAAAGAAAGTT 392
DB 7 LysProLysThrGluLysHisAspAlaHisGlyAlaGlyAsn----- 20
OY 393 TGTAAAGCTCTTCGGTATCTTGTGTGAAGGGCTATGTGGCTGACCGGAAGGTGAG 452
DB 21 -----GlyLeuAspGlyGlyLeuSerSerMetGlnGlyTrp 32
OY 453 AGGAGAGATGACAGATGCCACGTCATCTGAAACGATCAACGATCAACGAGAGTAAAGCCC 512
DB 33 ArgValGluMetGluAspAlaHisThrAlaValAlaGlyIle----- 46
OY 513 CCATGCGCCCTCATTAAGTCGGGTTTCATATTGTTGCTTTTGAATGACATGAGAAATT 572
DB 47 ProHisGlyLeu---GluAspTrpSerPhePheAlaValTYrAspGlyHisAlaGlySer 65
OY 573 CGAGCCCTCAAAATTTGTCGACAGATTTGCATCAAAACTTAATATGACA----- 620
DB 66 ArgValHisAsnTYrCySerThrHisLeuLeuGlnHisIleThrThrAsnGluAspPhe 85
OY 621 -----AAATTCCTAAAGAGATGTAAAGTGAAGTGAAGAAACCGTAAGAGA 668
DB 86 ArgAlaAlaGlyLysSerGlySerAlaLeuGluLeuSerValGlu---AsnValLysAsn 104
OY 669 TGCCTTTGACACTTTCAAGCATTCGATGAAGAGTTCCTTAAACAAGCTTCACGCGAG 728
DB 105 GlyIleArgThrGlyPheLeuLysIleAspIleuTYrMetArgAsnPheSerAspLeuArg 124
OY 729 AAGCTGCTCGAAGAGATGGTCCATGCGCACGCTGTTCTGGCTGTGAACAATCTT 788
DB 125 AsnGlyMetAspArgSerGlySerThrAlaValAlaGlyValMetIleSerProLysHisIle 144
OY 789 TATATGCCAACTCGAGATAGTGGGCAATCTTGTCGTATATATGAGAGAGTCAA 848
DB 145 TyrPheIleAsnCySglYAspSerArgAlaValLeuTYrArgAsnGlyIle----- 161
OY 849 AAACATGACACTTAAGCTTCAGCAAAAGCATATTCACCTCAGATATGAAGCGCATG 908
DB 162 -----ValCySpsSerThrGlnAspHisLysProCyAsnProArgGluLeu 178
OY 909 AGATATCGAAGAGCTGAGAGAAACGTCAAGGATGGCGTGTGTCGCTGACAGGTG 968
DB 179 ArgIleGlnAsnAlaGlyGlySerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
OY 969 TCACGCTCCATTGGGGAACGGCAGTACAAAGCCGTCGGT----- 1007
DB 199 SerAgaLaLeuGlyAspTYrAspTYrLysCyValAspGlyLysGlyProThrGluGln 218
OY 1008 ---GTCACCTCTGTGCCGACATACAGCCTCCAGCTGACCCCAATGACAGTTTCAT 1064
DB 219 LeuValSerProGluProGluValTYrGluIleLeuAraGluGluGluAspGluPheIle 238
OY 1065 TTGTTGGCTGTGATGGGCTCTTCAGGCTTTTACCCAGAAAGACCCGTAACCTCATC 1124
DB 239 IleLeuAlaCyAspGlyIleTrpAspValMetSerAraGluGluIleuCySgluTYrVal 258
OY 1125 TTGCTCTGTCTGAGATGAAGAATCCAGACCCGGAAAGGAGTCCGACGCCAGCC 1184
DB 259 LysSerArgLeuGlu-----ValSerAsp 266
OY 1185 CGCTACGAGCAGCCTGCAACAGGCTGCGCAACAGCCGTCGACGGGGCTGCGCCGAC 1244

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Db 267 AepLeuGluaenValCyseantPpValaPbThCyseuHiSlyeSlySerArgAsp 286
Qy 1245 AACGTCACTGTGATGGTGTG 1265
Db 287 AsnMetSerIleValLeuVal 293

RESULT 22
US-09-925-300-1655
; Sequence 1655, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1655
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (144)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (290)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (325)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1655

Alignment Scores:
Pred. No.: 1,49e-19 Length: 373
Score: 312.00 Matches: 112
Percent Similarity: 40.83 Conservative: 55
Best Local Similarity: 27.38 Mismatches: 128
Query Match: 12.198 Indels: 114
Gaps: 15

US-09-935-124A-1 (1-1422) x US-09-925-300-1655 (1-373)

Qy 180 CTGCTCTTTGATGAC-----CTCCCTCCGGCCAGCACTGTAAGTCA----- 221
Db 28 LeuLeuGlnAspAspArgValThrProThrCyHisSerSerThrSerGluProArg 47
Qy 222 -----GGATCAGGGGAGCTTTGGCTTTGATGAT----- 251
Db 48 CySerArgPheAspProAspGlySerGlySerProAlaThrTrpAspAsnPheGlyIle 67
Qy 252 -----CTCCACCCCGCTAGACAGTGGCGATTGAGGT 281
Db 68 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 82
Qy 282 TCTCTTGGCCATCATATATCCAGATGTTAAAGACTGAAGGGAAGGAAGCAAGAAAA 341
Db 82 ----- 82
Qy 342 ACCTCGAGAGAGAGAAGATGCGACGTGAAGAGCTTGTGAAAGAAAGTTGTTAAAGCC 401
Db 83 -----LysTyrGly-----LysProIleProIleProIle 91
Qy 402 TCTTCGGTATCTTTGGTGTGAAGGGCTATGTGCTGAGCGGAAGGGTGAAGAGGAGAG 461

Db 92 SerLeuGluAsnValGlyCyseAlaSerGlnIleGlyLysArgLys---GluAsnGluAsp 110
Qy 462 ATGCAGAGATGCCAGGTGATCTCTGAACGACATCACCGAAGATGAAGGCCCATCGTCC 521
Db 111 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 120
Qy 522 CTCATTAATCTCGGGTTTCATATTTCCTGTTTGTGATGACATGAGAGAAATTCAGACCTCA 581
Db 121 -----ValLeuTyrPheAlaValTyrAspGlyHisGlyGlyProAlaAlaAla 136
Qy 582 AAATTTCGTCACAGAAATTTGCTCAAACTTAATCAGAAAAATTTCTTAAGCAAGATGA 641
Db 137 AspPheCyHisThrHisIleMet**LysCysIleMetAspLeuLeuProLys----- 153
Qy 642 ATCAGGTGTAAGAAACCGTGAAGAGATGCCCTTTTGGACACTTGAAGATGATGATGA 701
Db 154 -----GlnLysAsnLeuGlnThrLeuLeuThrLeuAlaPheLeuGlnIleAspLys 170
Qy 702 GAGTTCCTTAAACAAGCT-----TCCAGCCGAAGCCCTGGAAAGATGGTCCACT 755
Db 171 AlaPheSerSerHisAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThrThr 190
Qy 756 GCCACGTGTGTTGCGCTGTAGACAACATT---CTTATATGCCAACCTCGAAGATAGT 812
Db 191 AlaThrValAlaLeuLeuArgAspGlyIleGlnLeuValAlaIleSerValGlyAspSer 210
Qy 813 CGGGCAATCTGTGTGGTATATGATGAGAGAGTCAAAACATGACGCCCTTAAGCCTCAGC 872
Db 211 ArgAlaIleLeuCyArg-----LysGlyLysProMetLysLeuThr 224
Qy 872 AAAGACATATCTCACTACATGATGAGAGAGCGAGATGAGATGACAGAAAGCTGAGAGA--- 929
Db 225 IleAspHisThrProGlnArgLysAspGlyLysGlnArgIleLysLysCysGlyGlyPhe 244
Qy 930 -----ACGTCAAGGATGCGCGTGTTTGGCGCTCTTAAGGTGTCAGCTCC 977
Db 245 ValAlaTrpAsnSerLeuGlyGlnProHisValAsnGlyArgLeuAlaMetThrArgSer 264
Qy 978 ATTTGGGAGCGGCAGTACAGAGCGCTGCGCTGACCTGTGCGGACATGACAGCTGTC 1037
Db 265 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGluThrLysArgIle 284
Qy 1038 CAGCTG---ACCCCAATGACAGTTCATTTGTTGGCTGATGAGGCTTTCAGAGTTC 1094
Db 285 LysLeuHisHisAla**AspSerPheLeuValLeuThrThrAspGlyIleAsnIleMet 304
Qy 1095 TTTACCCCAAGAAAGACCGGTGACTTTCATTTGCTGCTGCTGCGAGATGAAGATCCAG 1154
Db 305 ValAsnSerGlnGluIleCysAspPheValAsnGlnCyHisIleAspProAsnGlu----- 322
Qy 1155 ACCCGGAAGGGAAGTCCGACCGACCGCCGCTGAAGAGCACTGCAACAGGCTGGCC 1214
Db 323 -----AlaAla**AlaVal** 328
Qy 1215 AACAGCGGTGACAGCGGGCTCGGCCGACATGACTGTGATGCTGTCGGATGAGG 1274
Db 329 GlnGlnAlaIleGlnIleTyrGlyThrGluAspAsnSerThrAlaValValProIleGly 348
Qy 1275 CACTAGAGGGGTGGCGCGGCGGACAGAG 1301
Db 349 AlaTrpGlyLysTyrLysAsnSerGlu 357

RESULT 23
US-09-925-300-1254
; Sequence 1254, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300


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Qy 516 TCGTCCCTCATTAAGTGGGTTTCATATTTTCTGTTTGTATGACATGAGAAATTCGA 575
Db 52 GATTPALALEU-----PheAlaValIleuAspGlyHisGlyAlaArg 66
Qy 576 GCGTCAAAATTTGCTGCACAGAAATTTGCATCAAACTTATTCAGAAATTTCTTAAAGA 635
Db 67 AAlaAlaArgPheGlyAlaArgHisLeuProGlyHisValIleuGlnIleu-----Gly 84
Qy 636 GATGTAATCATGATGAGAAACCGTGAAGATGCTTTTGGACACTTTCAGACTACT 695
Db 85 ProGluProSerGluProIleuGlyValArgGluAlaLeuArgAlaPheLeuSerAla 104
Qy 696 GATGAAGACTTCTTAAACAGCTTCACCGACAGAGCTGCTG-----AAA 743
Db 105 AspGluArgLeu-----ArgSerLeuTrpProArgValGluThr 117
Qy 744 GATGGTCCATGCGCCACGCTGTGCTGCTGATGACAACTTATTTATTCGCAACCTC 803
Db 118 GlyGlyPheThrAlaValIleuLeuValSerProArgPheLeuValHisCys 137
Qy 804 GGAGATAGTCGGGCAATCTTGTCCTTATTAATGAGAGATCAAAACATGACAGCTTA 863
Db 138 GlyAspSerArgAlaValLeu-----SerArgAlaGlyAlaValAla 151
Qy 864 AGCTTCAGCAAGACATTAATCCAACTCAGTATGAAGACCGAGATGAGATACAGAGCT 923
Db 152 PheSerThrGluAspHisArgProLeuArgProArgIleuArgIleHisAlaAla 171
Qy 924 GGAGAAAGCTCAGGATGCGCTGTTTGGGCTGCTAGAGTGTCAAGCTTCATTTGG 983
Db 172 GlyGlyThrIleArgArgArgValGlyGlySerLeuAlaValSerArgAlaLeuGly 191
Qy 984 GACGGCAGTACAGAGCGCTGCGGT-----GTCACTCTGTG 1019
Db 192 AspPheThrTyrLeuGluAlaProGlyArgProProGluLeuGlnLeuValSerAlaGlu 211
Qy 1020 CCGCAGATCAGACGCTGCAGCTGACCCCAATGACAGGTTTATTTGTGGCTGTGAT 1079
Db 212 ProGluValAlaAlaLeuAlaArgGlnAlaGluAspGluPheLeuLeuAlaSerAsp 231
Qy 1080 GGGCTCTTCAAGTCTTATCCCAAGAAAGCCGTGAATCTTATCTTGTCTCTCGAG 1139
Db 232 GlyValTTPAspThrValSerGlyAlaAlaLeuAlaGlyLeuValAlaSerArgLeu 250
Qy 1140 GATGAAGAATCCAGACCGCGGAAGGAGTCCGACCGCAGCGCCGCTACAGAGCGC 1199
Db 251 -----ArgLeuGlyLeuAlaPro-----GluLeuLeu 259
Qy 1200 TGCACAGCTGCGCCACAGAGCGGTGACGCGGCTCGCGCAGCAACGTCATGTGATG 1259
Db 260 CysAlaGlnLeuLeuAspThrCysLeuGlySerLeuAspMetThrCysIle 279
Qy 1260 GTGGTCCGATGAGGACATGAGGGGTGGCGCGCGCAGAGACGCAATGATTAATT 1319
Db 280 LeuValCysPhePro-----GlyAlaProArgProSerGluGlnAla-----Ile 294
Qy 1320 AAAAGTTCATT-----TTGTGTGTGTCACATGTGTGTTTGTGTAATCTCT 1367
Db 295 ArgAlaGlnLeuAlaLeuAspAlaAlaLeuGlyCysArgIleAlaGluLeuValSer 314
Qy 1368 GTGGGACTCCA 1379
Db 315 AlaGlnIlePro 318

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; FILE REFERENCE: 38155-20013.00
; CURRENT APPLICATION NUMBER: US/09/860,351
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,260
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-860-351-2

Alignment Scores:
Pred. No.: 5,31e-17 Length: 352
Score: 283.00 Matches: 100
Percent Similarity: 41.93% Conserved: 48
Best Local Similarity: 28.33% Mismatches: 107
Query Match: 11.05% Indels: 98
Gaps: 14

US-09-935-124a-1 (1-1422) x US-09-860-351-2 (1-352)

Qy 180 CTGCTCTTTGATGAC-----CTCCCTCGGCGCAGCAGTACTGACTCA----- 221
Db 27 LeuLeuGlnAspAspArgArgValThrProThrCysHisSerSerThrSerGluProArg 46
Qy 222 -----GGATCAGGGGACCTTTGCTTTTGTATGAT----- 251
Db 47 CysSerArgPheAspProAspGlySerGlySerProAlaThrTTPAspAsnHeGlyIle 66
Qy 252 -----CTCCACCGCGCTAGCAGTGGCGATTCAAGT 281
Db 67 TrpAspAsnArgIleAspGluProIleLeuLeuProProSerIle----- 81
Qy 282 TCTCTTGCCACATCAATATCCAGATGTAAGACTGAAGGAAAGAGCAAAAGAAAA 341
Db 81 ----- 81
Qy 342 ACCTCGAGAGAGAGAAATGCGACGTGAAGACTTGTGAAAGATTGTAAAGCC 401
Db 82 -----LysTyrIle-----LysProIleProIle 90
Qy 402 TCTTGGTATCTTGTGCTGAAGGCTATGAGCTGACGCGAGAGGTGAGAGAGAG 461
Db 91 SerLeuGluAsnValGlyCysAlaSerGlnIleGlyIleArgGlyIle-----GluAsnGluAsp 109
Qy 462 ATGACAGATGCCACATCTGTAACGACATCACCGAGAGGTGAGGCCCATCGTCC 521
Db 110 ArgPheAsp-----PheAlaGlnLeuThrAspGlu----- 119
Qy 522 CTCATTATCTCGGCTTCAATATTTGCTGTTTGAATGACATGAGAAATTCGAGCTCA 581
Db 120 -----ValLeuTyrPheAlaValIleValIleArgGlyIleGlyIleProAlaAlaAla 135
Qy 582 AAATTGCTGCACAGAAATTTGCATCAAACTTATTCAGAAATTTCTTAAAGAGATGA 641
Db 136 AspPheCysHisThrHisMetGlyCysIleMetAspLeuLeuProIle----- 152
Qy 642 ATCAGTGAAGAAAAACGTGAAGAGATGCTTTTGAACATTTCAACATATCTGATGA 701
Db 153 -----GluTyrAsnLeuGlnThrLeuLeuThrIleAlaPheLeuGlnIleAspIle 169
Qy 702 GAGTTCCTTAAACAGCT-----TCCAGCCAGAGCCTGCTGAGAAAGATGGTCCACT 755
Db 170 AlaPheSerSerHisAlaArgLeuSerAlaAspAlaThrLeuLeuThrSerGlyThr 189
Qy 756 GCCACGTGTGTTGCTGCTGATGACAACTT-----CTTATATTCGCAACCTCGAGATAGT 812
Db 190 AlaThrValAlaLeuLeuArgAspGlyIleGluLeuValAlaHisValGlyAspSer 209
Qy 813 CCGGCAATCTTGTGCTTATTAATGAGAGAGTCAAAACATGACGCTTAAGCTCAGC 872

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Db 210 ArgAlaIleLeuCysArg-----LysGlyLysProMetLysLeuThr 223
QY 873 AAAGAGCAATATCCAACTCACTATGAAGACGGATGAGATACAGAGCGCTGGAGGA--- 929
Db 224 IleAspHisThrProGluArgLysAspGluLysGluArgLysCysGlyGlyPhe 243
QY 930 -----AACGTACGGAGATGGAGCGGTGTTGGCGGTGCTAAGAGTGTCAACCTGC 977
Db 244 ValAlaTrpAsnSerLeuGlyGlnProHisValAsnGlyArgLeuAlaMetTrpArgSer 263
QY 978 ATTGGGACGGGCACTACAAGCGCTGGCTGTCACTGTGTGCCGACATCAGACGCTGC 1037
Db 264 IleGlyAspLeuAspLeuLysThrSerGlyValIleAlaGluProGluThrLysArgIle 283
QY 1038 CAGCTG---ACCCCAATGACAGGTTCAATTTGTGGCCTGTGATGGGCTCTTCAAGATC 1094
Db 284 LysLeuHisHisIleAlaAspAspSerPheLeuValIleuThrThrAspGlyIleAsnPheMet 303
QY 1095 TTACCCCAAGAGACCGGCACTTCACTTGTCTGCTGT 1133
Db 304 ValAsnSerGlnGluIleCysAspPheValAsnGlnCys 316
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Search completed: February 9, 2003, 18:12:41
Job time : 37.5 secs

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/ NUMBER OF SEQ ID NOS: 2318
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1562
/ LENGTH: 441
/ TYPE: PRT
/ ORGANISM: Homo sapiens
PCT-US01-01239-1562

Alignment Scores:
Pred. No.: 5,32e-171 Length: 441
Score: 2199.00 Matches: 423
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.90% Indels: 0
DB: 1 Gaps: 0

US-09-935-124A-1 (1-1422) x PCT-US01-01239-1562 (1-441)

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QY 69 TGTGCTGTGCGCGCGCTCCACCCAGCCTCCGCGAGTGAACCTTTCGGGGACCTGCGGAG 128
DB 39 CySaRgCySaRgLeuHISProAlaSerAlaMetAspLeuPheGlyAspLeuProGlu 58
QY 129 CCGAGCGCTGCGCGCGCGCGCTGCGCGGAAAGAGCTCAGAAAGACCCCTGCTCTT 188
DB 59 ProGluARgSerProARgProAlaIaGlyLyGluAlaGlnLySerGlyProLeuLeuPhe 78
QY 189 GATGACCTCCCTCCGCGCAGCAGTACTGACTCAGATCAGGGGACCTTTCCTTTGAT 248
DB 79 AspAspLeuProProAlaSerSerThrAspSerGlySerGlyProLeuLeuPheAsp 98
QY 249 GATCTCCGACCCGCTAGCAGTGGCGATTCAGTTCCTTTCGACATCAATATCCAGATG 308
DB 99 AspLeuProProAlaSerSerGlyAspSerGlySerLeuAlaHISerLieserGlnMet 118
QY 309 GTAAGACTGAAGGAAAGAGAGCAAGAAACCTCCGAGAGAGAGAGATGACAGT 368
DB 119 ValLySerThGlnGlyLySerGlyAlaLySerGlyThrSerGlnGlnGlnLySer 138
QY 369 GAAAGACTTGTGGAAGAAAGTTTGTAAAGCTTTCGCTGATCTTTCGCTGAGAGGC 428
DB 139 GluGlnLeuValGlnLySerValCyLySaLaserSerValIlePheGlyLeuLySer 158
QY 429 TATGTGCGTGAAGCGGAAGGTGAGAGGAGAGATGACAGAGTCCACGTCATCTCGAAC 488
DB 159 TyrValAlaGlnLySerGlyGlnLySerGlnGlnMetGlnAspAlaHISValIleLeuAsn 178
QY 489 GACATCACCAGAGAGTGTAGGCCCCCATCGTCCCTCATTAATCGGGTTTCATATTGCT 548
DB 179 AspLIEthThGlnGlnLySerARgPrProPserSerLeuIleThrARgValSerTyRPhaAla 198
QY 549 GTTTTGTGATGAGATGAGAGAAATTCAGACCTCAAAATTTGCTGACACAGAAATTTGACAA 608
DB 199 ValIAspGlyHISGlyGlyIleARgAlaSerLyPheAlaIaGlnAsnLeuHISGln 218
QY 609 AACTTAATCAGAAATTTCTTAAGAGATGTATATCAGTGTAGAGAAACCGTGAAGAGA 668
DB 219 AsnLeuHISARgLyPhePheProLySgIAspValIleSerValGlnLySerThrValIlySaRg 238
QY 669 TGCCTTTTGGACACTTCAAGCATACTGATGAAGATTCCTTAAACAGCTTCCAGCCAG 728
DB 239 CyLeuLeuAspThrPheLySerHISThrAspGlnGlnPheLeuLySgInAlaSerSerGln 258
QY 729 AAGCTGCTGGAAGAGATGAGTCACTGCCACGTTGTTCTGCGCTGAGAACAACTTCTT 788
DB 259 LySProAlaITrLyAspGlySerThrAlaThrCyValIleuHISValIAspLeuHISleu 278
QY 789 TATATTGCGCAACTCGGAGATAGTCCGGCAATTTGTGTCTTATTAATGAGAGATCAA 848
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QY 849 AAATATGACCTTAAAGCTCAGCAAGAGCATTAATCCAACTCAGTATGAAAGCGGATG 908
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QY 909 AGGATATCAGAAAGCTGAGAGAAACGTCAAGGATGGCGCTGTTTGGCGCTGCTAAGGTG 968
DB 319 ArgIleGlnLySaLagIyGlyAsnValIAspValIAspValIleuGlyValIleuGlyVal 338
QY 969 TCAGCTCCATTTGGGAGAGCGGAGATGACAGCGCTGCGGCTGACCTGTGTCGCCAGATC 1028
DB 339 SerARgSerIleGlyAspGlyGlnTyRlySaRgCySgIyValIthSerValIProAspIle 358
QY 1029 AGACGCTGCGACGTGACCCCAATGACAGTTTCATTTGTTGGCTGTGATGGGCTCTTC 1088
DB 359 ARgARgCyGlnLeuThrProAsnAspARgPheIleLeuAlaCyAspGlyLeuPhe 378
QY 1089 AAGTCTTTAACCCGGAAGAGCCGTGAACCTTCATCTTGTCTGTCTGAGAGATGAANG 1148
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QY 1149 ATCCAGACCCGGAAGGAGAGTCCGACGCCGCGCTACGAAAGACGCTGCAACAGG 1208
DB 399 ILeGlnThrARgGlnGlyLySerAlaAlaAspAlaARgTyRGlAlaAlaCySaRnARg 418
QY 1209 CTGGCCAAACAGCGCGTGCAGCGGCTCGGCCGACAACTGTCATGTGATGCTGTCGCG 1268
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QY 1269 ATAGGGCAC 1277
DB 439 ILeGlyHIS 441

RESULT 2
US-09-764-902-1562
/ Sequence 1562, Application US/09764902
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PT213
/ CURRENT APPLICATION NUMBER: US/09/764,902
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - refer to PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 2318
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 1562
/ LENGTH: 441
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-764-902-1562

Alignment Scores:
Pred. No.: 5,32e-171 Length: 441
Score: 2199.00 Matches: 423
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.90% Indels: 0
DB: 21 Gaps: 0

US-09-935-124A-1 (1-1422) x US-09-764-902-1562 (1-441)

QY 9 GCCCGCTGCTGCCCGCCCGGGGCTGTGAGCCCGCGCTGCTGCGGGCTGAGTGTTC 68
DB 19 AIAATGCGySaRgPrProGlyValITrPserProAlaAlaIaARgGlyLeuSerVal 38
QY 69 TGTGCTGTGCGCGCTCCACCCAGCCTCCGCGAGTGAACCTTTCGGGGACCTGCGGAG 128
DB 39 CySaRgCySaRgLeuHISProAlaSerAlaMetAspLeuPheGlyAspLeuProGlu 58
QY 129 CCGAGCGCTGCGCGCGCGCGCTGCGCGGAAAGAGCTCAGAAAGACCCCTGCTCTT 188
DB 59 ProGluARgSerProARgProAlaIaGlyLySgInAlaGlnLySerGlyProLeuLeuPhe 78
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QY 189 GATGACCTCCCTCGGCGACGACTGATCTCAGATCAGGAGGACCTTTGCTTTTGAT 248
 DB 79 AapAapLeuProProAlaSerSerThraSerSerGlySerGlyProLeuLeuPheasp 98
 QY 249 GATCTCCAGCCCGCTAGCGATGCGATTCAGGTTCTTTCGACATCAATATCCAGATG 308
 DB 99 AapLeuProProAlaSerSerGlyAapSerSerGlySerLeuAlaThraSerSerGlyMet 118
 QY 309 GTAAGAAGCTGAAGGAAAGAGCAAGAGAAAACCTCCAGAGAGAGAGATGCGAT 368
 DB 119 ValValThraGluGlyGlyGlyAlaValSerGlyThraSerSerGluGluValSerGlySer 138
 QY 369 GAAGAGCTTGAG 428
 DB 139 GluGluLeuValGluValGlyValGlyValGlyValSerSerValIlePheGlyLeuGly 158
 QY 429 TATGAGCTGAGCGGAG 488
 DB 159 TyrValAlaGluValGlyGlyGlyValGluGluMetGluAlaIleValIleLeuAla 178
 QY 489 GACATCAGCGAG 548
 DB 179 AspIleThraGluGluGlyAapGlyProSerSerLeuIleThraGlyValSerTyPheAla 198
 QY 549 GTTTTGTATGACATGAGAGAGATTCAGGCTCAAAATTTGCTGCACGAGATTTGCATCA 608
 DB 199 ValPheaspGlyThraGlyGlyIleAapAlaSerTyPheAlaAlaGluAlaMetLeuIleGln 218
 QY 609 AACTTAATCAGAGAAATTTCTTAAGAGAGATGTAATCAGTGAAGAGAAACCTGGAAGAA 668
 DB 219 AsnLeuIleAapGlyPhePheProGlyAapValIleSerValGluValThraValPheArg 238
 QY 669 TGCCTTTTGAGACACTTTCAAGCATATCATGATGAAGAGATTCCTTAAACAGGTTCCAGCCAG 728
 DB 239 CysLeuLeuAapThraPheValIleThraAapGluGluPheLeuValGlnAlaSerSerGln 258
 QY 729 AAGCGTCCGGAAGAGATGAGTCACTGCCAGCTGTGTTCTGCGTGTGAACAATTTCTT 788
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 QY 789 TATATGCGCAAGCTCGAGATAGTGGGCAATCTTGCTGTGTTATTAAGAGAGAGTCAA 848
 DB 279 TyrIleAlaAsnLeuGlyAapSerThraIleLeuCysArgTyPheGluGluSerGln 298
 QY 849 AAAAGTCAGCCTTAAGCCTCGAGAGAGAGATTAATCGCAACTCAGATGAAGAGAGCGATG 908
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 DB 319 ArgIleGlnValAlaGlyIleValSerValAapGlyAapGlyValAlaLeuGluVal 338
 QY 969 TCACGCTTCATTGGGAGCGGCGAGTGAACAGGCTGCGGTGTCACTCTGTGCCGACATC 1028
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 QY 1089 AAGGCTTTTATCCCGAG 1148
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 QY 1149 ATCCAGACCCGAG 1208
 DB 399 IleGlnThraArgGluGlyLysSerAlaAlaPheAlaArgTyGluAlaAlaCysAsnArg 418
 QY 1209 CTGGCCACAG 1268
 DB 419 LeuAlaAsnValAlaValAlaGluValGlySerAlaAapValAlaThraValMetValValArg 438
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DB 439 IleGlyHis 441
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 PCT-US01-01239-929
 / Sequence 929, Application PC/TUS0101239
 / GENERAL INFORMATION:
 / APPLICANT: Human Genome Sciences, Inc., et al.
 / TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 / FILE REFERENCE: P71213PCT
 / CURRENT APPLICATION NUMBER: PCT/US01/01239
 / PRIOR APPLICATION DATA: 2001-01-17
 / Prior application data removed - refer to PALM or file wrapper
 / NUMBER OF SEQ ID NOS: 2318
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 929
 / LENGTH: 446
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 PCT-US01-01239-929
 Alignment Scores:
 Pred. No.: 5,34e-171 Length: 446
 Score: 2199.00 Matches: 423
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.90% Indels: 0
 DB: 1 Gaps: 0
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 QY 69 TGTCCGCTGCGAG 128
 DB 44 CysArgCysCyahArgProAlaSerAlaMetAapLeuPheGlyAapLeuProGlu 63
 QY 129 CCCGAGCGCTGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTT 188
 DB 64 ProGluArgSerProArgProAlaSerAlaGlyValGluAlaGlnGlyProLeuLeuPhe 83
 QY 189 GATGACCTCCCTCGGCGAGAGTCACTGACTCAGATCAGAGGGGACCTTTCCTTTTGAT 248
 DB 84 AapAapLeuProProAlaSerSerThraAapSerGlySerIleAlaThraSerIleSerGlnMet 103
 QY 249 GATCTCCAGCCCGCTAGAGTGGCGATTCAGGTTCTTTCGACATCAATATCCAGATG 308
 DB 104 AapLeuProProAlaSerSerGlyAapSerGlySerLeuAlaThraSerIleSerGlnMet 123
 QY 309 GTAAGAAGCTGAAGGAAAGAGCAAGAGAAAACCTCCAGAGAGAGAGAGAGATGCGAGT 368
 DB 124 ValIleThraGluGlyGlyGlyAlaValSerGlyThraSerSerGluGluValAlaSerGly 143
 QY 369 GAAGAGCTTGAG 428
 DB 144 GluGluLeuValGluValGlyValGlyValGlyValSerSerValIlePheGlyLeuGly 163
 QY 429 TATGAGCTGAG 488
 DB 164 TyrValAlaGluValGlyGlyGlyValGluGluMetGluAlaIleValIleLeuAla 183
 QY 489 GACATCAGCGAG 548
 DB 184 AspIleThraGluGluGlyAapGlyProSerSerLeuIleThraArgValSerTyPheAla 203
 QY 549 GTTTTGTATGACATGAGAGAGATTCAGGCTCAAAATTTGCTGCACGAGATTTGCATCA 608
 DB 204 ValPheaspGlyThraGlyGlyIleAapAlaSerTyPheAlaAlaGluAlaMetLeuIleGln 223
 QY 609 AACTTAATCAGAGAAATTTCTTAAGAGAGATGTAATCAGTGAAGAGAAACCTGGAAGAA 668

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Db      224 AsnLeuIleArgLysPheProLysGlyAspValIleSerValGluLysThrValLysArg 243
Qy      669 TGCCTTTGAGACCTTTCAGCATCTGATGAAGAGTCTCTTAAGACCTTCCAGCCAG 728
Db      244 CysLeuLeuAspThrPheLysHisThrAspGluLysPheLeuLysGlnLysSerGln 263
Qy      729 AAGCTGCTGGAAAGATGGGTCCACTGCCAGCTGTGTTCTGGCTGTAGCAACATTCTT 788
Db      264 LysProAlaTrpLysAspGlySerThrAlaThrCysValLeuAlaValAspAsnIleLeu 283
Qy      789 TATATTGGCAACCTGGAGATGTCGGGCAATCTTGTCGTTATATATAGAGAGATGCA 848
Db      284 TyrIleAlaAsnLeuLysAspSerArgAlaIleLeuCysArgGlyAsnGluLysSerGln 303
Qy      849 AAGCATGCAAGCTTAAAGCTTCAGCAAAAGACATATCCAACTCAGTATGAAGCGCATG 908
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Qy      909 AGGATTCAGAAAGGCTGAGGAAAGCTCAGGAGATGGCGCTGTTTGGCGCTGTAGAGTGG 968
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Qy      969 TCACGCTTCATTTGGGAGCGGAGCTGACAGCGCTGGGTGTCACTCTGCCCCGACATC 1028
Db      344 SerArgSerIleGlyAspGlyGlnTyrLysArgCysGlyValThrSerValProAspIle 363
Qy      1029 AGACGCTGCAGCTGACCCCAATGACAGTTTCATTTGTTGGCTGTAGAGGCTCTTC 1088
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Qy      1089 AAGCTTTTATCCCAAGAAAGCGTGAACCTTCATCTTGTCTGTCTGAGATGAAAG 1148
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Qy      1149 ATCCAAACCCGGGAAGGAAGTCCGACGCGGACGCGCTGACAAACACCTTCGCAACAG 1208
Db      404 TleGlnThrArgGluGluLysSerAlaAlaAspAlaArgTyrGluAlaAlaCysAsnArg 423
Qy      1209 CTGGCCCAAGGCGGTGACGCGGCTGCGGCGGCAAGTCACTGATGTGTGGTGGCG 1268
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RESULT 4
US-09-764-902-929
; Sequence 929, Application US/09764902
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT213
; CURRENT APPLICATION NUMBER: US/09/764,902
; PRIORITY FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2318
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 929
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-902-929

Alignment Scores:
Pred. No.: 5,346-171 Length: 446
Score: 2199.00 Matches: 423
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.90% Indels: 0
Db: 21 Gaps: 0
US-09-935-124A-1 (1-1422) x US-09-764-902-929 (1-446)

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Qy      9 GCCCGCTGTCGCGCCGCGCGGGGTGTGAGCCCGGCGCTGCTCGCGGCTGAGTGC 68
Db      24 AlaArgCysArgProProGlyValTrpSerProAlaAlaAlaArgGlyLeuSerVal 43
Qy      69 TGTCCGTGTCGCGCTGACCCAGCCAGCTCCCGCATGACCTTTGGGGACCTGCCGAG 128
Db      44 CysArgCysArgLeuHisProAlaSerAlaMetAspLeuPheGlyAspLeuProGlu 63
Qy      129 CCGGAGCGTGGCGCGCGCGCTGCGGAAAGAAAGCTCGAAAGAGCCCTGCTCTT 188
Db      64 ProGluArgSerProAlaTrpAlaIleGlySerGluAlaGlnLysGlyProLeuLeuPhe 83
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Db      84 AspAspLeuProProAlaSerSerThrAspSerGlySerGlyProLeuLeuPheAsp 103
Qy      249 GATCTCCACCCGCTGAGAGTGGGCAATTCAGGTTCTTTGCCATCAATATCCAGATG 308
Db      104 AspLeuProProAlaSerSerGlyAspSerGlySerLeuAlaThrSerIleSerGlnMet 123
Qy      309 GTAAAGACTGAAAGGAAAGAGCAAAAGAAAGAAACCTCCGAGAAAGAGAAAGATGCACT 368
Db      124 ValLysThrGluGlyLysGlyAlaLysArgLysThrSerGluGluLysAsnGlySer 143
Qy      369 GAAGAGCTTGTGAAAGAAAGATTGTAAAGCTCTTCGATGATCTTGTGCTGAAAGGC 428
Db      144 GluGluLeuValGluLysLysValCysLysAlaSerSerValIlePheGlyLeuLysGly 163
Qy      429 TATGTGCTGACAGCGGAGGAGTGAAGGAGAGATGACAGATGCCACATCATCTTAAC 488
Db      164 TyrValAlaGluArgLysGlyGluLysGluGluMetGlnAspAlaHisValIleLeuLys 183
Qy      489 GACATCACCGAGAGATGTAAGGCCCCATCGTCCCTTACCTCGGGGTTCTATATTGCT 548
Db      184 AspIleThrGluGluCysArgProProSerSerLeuIleThrGlyValSerTyrPheAla 203
Qy      549 GTTTTGTATGACATGAGAGAAATTCGACCTCAAAATTTGCTGCAACAAATTTGCATCA 608
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Db      224 AsnLeuIleArgLysPheProLysGlyAspValIleSerValGluLysThrValLysArg 243
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Qy      789 TATATTGGCAACCTGGAGATGTCGGGCAATCTTGTCGTTATATATAGAGAGATGCA 848
Db      284 TyrIleAlaAsnLeuLysAspSerArgAlaIleLeuCysArgGlyAsnGluLysSerGln 303
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Qy      969 TCACGCTTCATTTGGGAGCGGAGCTGACAGCGCTGGGTGTCACTCTGCCCCGACATC 1028
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QY 1089 AAGCTTTTACCCGAGAGAGCCGTGAATTGCTTGTCTGTCAGAGATGAAAAG 1148
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QY 1209 CTGGCCAAACAGGCGGTGTCAGCGGGGCTCGCGGACAGACGTCTGATGTGTGGCG 1268
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QY 1269 ATAGGCAC 1277
DB 444 IIEGLYHIs 446

RESULT 5
PCT-US01-03800A-2687
; Sequence 2687, Application PC/TUS0103800A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: PCT/US01/03800A
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO: 2687
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-03800A-2687

Alignment Scores:
Pred. No.: 2,04e-166 Length: 421
Score: 2143.00 Matches: 414
Percent Similarity: 100.00% Conservative: 414
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.71% Indels: 0
Gaps: 0

US-09-935-124a-1 (1-1422) x PCT-US01-03800A-2687 (1-421)

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QY 96 TCCGCCATGGAACCTCTTGGGGAGCTGCGCGAGCCCGAGCGCTCGCCGCGCGCTGCC 155
DB 28 SerLametrAspLeuPheGlyAspLeuProGluArgProGluArgProAlaAla 47
QY 156 GGGAAAGAACTCAGAAAGAACCCCTGCTTTTGATGACCTCCCTCCGGCAGAGTACT 215
DB 48 GlyysGluAlaGlnLyysGlyProLeuLeuPheAspAspLeuProProAlaSerSerThr 67
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QY 276 TCAGGTTCTCTGTCACATCATATATCCAGATGTAAAGCTAAAGGAAAGGAGCAAG 335
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QY 336 AGAAAAACCTCCAGAGAGAGAAAGATGCGAGTGAAGGCTTGTGAAAGAAAGATTGT 395
DB 108 ArgysThrSerGluGluGluLysAsnGlySerGlnLysLeuValGlnLysLysValCys 127
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DB 128 LVyAlaSerSerValIlePheGlyLeuLyysGlyTrValAlaGlnAlaGlyysGlyGlnArg 147
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DB 208 AspValIleSerValGlnLyysThrValLyysArgCysLeuLeuAspTrnPheLyysIleTrn 227
QY 696 GATGAGAGTTCCTTAAACAGCTTCCAGCCAGAACCTTGCGAAGATGGGCTCCACT 755
DB 228 AspGluGluPheLeuLyysGlnAlaSerSerGlnLyysProAlaTrpLyysAspGlySerThr 247
QY 756 GCCACGATGTTCTGCTGTAGACACATCTTATATATGCCAACCTGAGATAGTCGG 815
DB 248 AlArhCysValIleuAlaValAspAsnIleuTrpIleAlaAsnLeuGlyAspSerArg 267
QY 816 GCATCTGTGTGCTTATATATGAGAGAGTCAAAACATGACGCTTAAGCCTCAGCAAA 875
DB 268 AlAlaLeuCyAsArgTrpAsnGluSerGlnLyysIleAlaAlaLeuSerLeuSerLyys 287
QY 876 GAGCATTAACCAATCAGTATGAGAGAGCGATGAGATGACAGAAAGCTGAGAAAGTGC 935
DB 288 GlnHisAsnTrnGlnTrnGlnGluGluArgLyysGlnLyysAlaGlyGlyAsnVal 307
QY 936 AGGATGCGCGCTTTTGGCGGTGCTGAGAGTGTCAACGCTCCATGAGGAGAGGCGCACTAC 995
DB 308 ArgAspGlyArgValLeuGlyValLeuGlnValSerArgSerIleLyysAspGlyGlnTrp 327
QY 996 AAGCGTGGCGGTGTCACCTGTGTGCCGACATGACAGCTGCCAGCTGACCCCAAGAC 1055
DB 348 ArgPheIleLeuLeuAlaCysAspGlyLeuPheLyysValPheTrpProGluGlnAlaVal 367
QY 1116 AACTTCATCTTGTCTGCTCGAGAGTGAAGATCCAGACCCGGGAAAGGAGATCCGCA 1175
DB 368 AsnPheIleLeuSerCysLeuGlnAspGluLysIleGlnThrArgGluGlyLyysSerAla 387
QY 1176 GCCAGAGCCCGCTAGAGAGACAGCTGCAAGAGCTGCGCAACAGCGGTGACGCGGCGC 1235
DB 388 AlaAspAlaArgTrpGlnAlaAlaCysAsnArgLeuAlaAsnLyysAlaValGlnArgGly 407
QY 1236 TCGGCCCAAGAGTCACTGTATGTGTGGTGGGATAGGCGAC 1277
DB 408 SerAlaAspAsnValTrnValMetValAlaArgIleGlyHis 421

RESULT 6
US-09-488-725A-5486
; Sequence 5486, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
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1 PRIOR FILLING DATE: 2000-06-20
2 PRIOR APPLICATION NUMBER: US09/620,312
3 PRIOR FILLING DATE: 2000-07-19
4 PRIOR APPLICATION NUMBER: US09/653,450
5 PRIOR FILLING DATE: 2000-08-31
6 PRIOR APPLICATION NUMBER: US09/662,191
7 PRIOR FILLING DATE: 2000-09-14
8 PRIOR APPLICATION NUMBER: US09/693,036
9 PRIOR FILLING DATE: 2000-10-19
10 PRIOR APPLICATION NUMBER: US09/727,344
11 PRIOR FILLING DATE: 2000-11-29
12 NUMBER OF SEQ ID NOS: 7144
13 SOFTWARE: pc FL_versions 1.0
14 SEQ ID NO 5486
15 LENGTH 421
16 TYPE: PRT
17 ORGANISM: Homo sapiens
18 OS-09-488-725A-5486

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Alignment Scores:		
Pred. No.:	2,04e-166	4
Score:	213.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	83.71%	Indels:
Ds:	18	Gaps:

Qy	36	TCGAGCCCGGCGCGTGCCTGGGGGCTGATGTCCTGTCGCTGCCTGCCTCAACCCAGGC	95
Db	8	TtptserProAlaAlaAlaAlaGlyLeuSerValCysArgCysCysAlaGlyLeuHisProAla	27
Qy	96	TCGCCCATGAACCTTTCTGGGGAACCTGCCTGGAGCCCGAGCGCTGCCTGGCGGCTGCC	155
Db	28	SerAlaMetAspLeuPheGlyAspLeuProGluProGluArgSerProArgProAlaAla	47
Qy	156	GGGAAGAAGCTCGAAGAAAGAACCCCTGCTCTTTGATATGACCTCCCTCGCGGACAGACT	215
Db	48	GlyIlybGlyAlaGlyIlybGlyProLeuLeuPheAspAspLeuProProAlaAspSerThr	67
Qy	216	GACTCAGGATCAGGGGGGACCTTTGCTTTTATGATATCTCCACCCGCTAGCAGTGGCAT	275
Db	68	AspSerGlySerGlyGlyProLeuLeuPheAspAspLeuProProAlaAspSerGlyAsp	87
Qy	276	TCAGGTTCTTTGCCACATCAATATCCAGATGGTAAAGACTGAAGGAAAGACCAAG	335
Db	88	SerGlySerLeuAlaThrSerLysSerGluMetValIlybThrGluGlyIlybGlyAlaIlys	107
Qy	336	AGAAAAACCTCCGAGGAAGAGAAAGATGGCGTGAAGAGCTTGAGAAAGAAAGTTGT	395
Db	108	ArgLysThrSerGlyGlyGlyIlybAlaIlybAlaMetLysSerGluGluLeuValGlyIlybLysCys	127
Qy	396	AAAGCTTCTCGGTGATCTTTGGTCTGAAGGCTATGGCTGACCGGAAGGGGTGAGAG	455
Db	128	LysAlaSerSerValIlePheGlyLeuSerGlyIlybAlaAlaGlyIlybGlyIlybAlaArg	147
Qy	456	GAGGAGATGACGAGATGCCCAAGTATCTTGAACGACATCACCGAGAGTGAAGCCCCCA	515
Db	148	GluGluMetGlnAspAlaAlaIleValIleLeuAlaAspIleThrGluGluCysValArgProPro	167
Qy	516	TCGTCCTCATTAACCTCCGGGTTTCATATTCTGTTTATGAGATGAGAGAAATCSA	575
Db	168	SerSerLeuIleThrArgValSerTyrPheAlaValPheAspGlyHisGlyIleArg	187
Qy	576	GCTTCAAAATTTGCTGCACAGAAATTTGCATCAAAATTAAACAGAAATTTCCCTAAAGA	635
Db	188	AlaSerLysPheAlaAlaGlyIleAspLeuHisGlyIleAspLeuIleArgLysPheProLysGly	207
Qy	636	GATGTATCACTGTATGAGAAACCTGTAAGATGCTTTTGGACATCTTTCAGACATACT	695
Db	208	AspValIleSerValGlyLysThrValLysArgCysLeuLeuAspThrPheLysHisThr	227

QY	696	GATGAAGATGCTCTTAAACAAGCTTCACACGAAGACCGCTGGAAAAGATGGGTCACCT	755
Db	228	ASpGIuInJhLeuEuYbGInLaIaSeSerGInLpSPoAlaTrpLYaSPoLYSeThr	247
QY	756	GCCACGCTGTTCGTGCGCTGAGACAACATCTCTTTATTAATGCGCAACTCGGAGATAGTCGG	815
Db	248	AlaThrCYaValLeuLaIaValaPhePenIleLeuYrIleAlaIaLeuGCLYAspSerArg	267
QY	816	GCAATCTTGTGTGCTTATTAATGAGAGAGCTCAAAAAATGCAGCCTTAACTTCAGCAA	875
Db	268	AlaIleLeuCYaArgYrXaNGInGInSeSerGInLYSHIaIaAlaLeuSerIeSeuSerLYs	287
QY	876	GAGCATATCAACCTCAGATGTGAAGCGGAGAGATACAGAAAGCGTGAGAAACGTC	935
Db	288	GLuHISaSProThrGInTrGInTrGInuAGMeCArgIleGInLYaIaGLYLYaSPaVal	307
QY	936	AGGAGTGGCGCTTTTGGCGCGCTGACGAGAGCTGACGCTCCATTTGGGGAGAGCGGCAGTAC	995
Db	308	ArgaSPoLYaArgValLeuGLYValLeuGLYValaSerArgSerIleGLYLYaSPoLYGInTr	327
QY	996	AAAGCGCTGCGGTGTCACTCTGTGTGCCCGACATCAGACGCTGCAGCTGACCCCAATGAC	1055
Db	328	LYaArgCYaGLYAlaThrSeValProaSPeIleArgArgCYaGInLeuThrProaSPaSP	347
QY	1056	AGGTATATTTTGTGGCGCTGATATGGGGCTTCAAGGTCTTTTAAACCCAGAAAGAGCGGTG	1115
Db	348	ArgPheIleLeuLeuLaIaCYaSPaSPGLYLeuPheLYaValPheThrProGLYInuLaIaVal	367
QY	1116	AACTTCATCTTGTCTGTCTGCTCGAGATGAAAAGATCCAGACCCGGGAAGGGAAAGTCCGCA	1175
Db	368	AsnPheIleLeuSerCYaSeuGLYLaSPeInuLYbIleGInThrArgGLYInuLYySeSerLa	387
QY	1176	GCCGACGCCCGCTACAGAGACGCTTSCAACAGCGTGGCCACAGAGCGGTGACAGCGGCGC	1235
Db	388	AlaSPaValaArgYrGLYInuLaIaIaCYaSPaSPaArgLeuLaIaSPaValaGLaValGLaArgGLY	407
QY	1236	TCGGCGGACAAAGTCACTGAGATGGTGGTGGCGGAGTAAAGGGCAC	1277
Db	408	SeValaSPaSPaValThrValMeCValaValaGLYIleGLYLYaS	421

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RESULT 7
PCT-US02-12341-2
Sequence 2: Application PC/TUS0212341
GENERAL INFORMATION:
APPLICANT: Lorens, James B.
APPLICANT: Xu, Weiduan
APPLICANT: Atchison, Robert E.
APPLICANT: Bogenberger, Jakob
APPLICANT: Rigel Pharmaceuticals, Incorporated
TITLE OF INVENTION: Modulators of Angiogenesis
FILE REFERENCE: 021044-000210PC
CURRENT APPLICATION NUMBER: PCT/US02/12341
CURRENT FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: US 60/284,760
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 09/935,124
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 392
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: C1-angiogenesis protein, integrin-linked kinase
OTHER INFORMATION: associated protein (ILKAP)
PCT-US02-12341-2

Alignment Scores:
Pred. No.: 3, 53e-156 length: 392
Score: 2018.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 78.83% Indels: 0 Gaps: 0
US-09-935-124A-1 (1-1422) x PCT-US02-12341-2 (1-392)
QY 102 ATGGAACCTTTCGGGAGACCTGCGGAGCCCGCTGCGCGCGCGCGCGCGGAA 161
DB 1 MetAspLeuPheGlyAspLeuProGluPheGlySerProAlaAspGlyAsp 20
QY 162 GAAGCTCAGAAAGAACCCCTGCTCTTTGATGACCTCCCTCGGCGACGATCACTCA 221
DB 21 GluAlaGlnLysGlyProLeuLeuPheAspLeuProProAlaSerSerThrAspSer 40
QY 222 GGATCAGGGGACCTTGTCTTTTGTGATGATCTCCACCCGCTGACAGTGGCATTCAGGT 281
DB 41 GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerSerGlyAspSerGly 60
QY 282 TCTCTGGCCACATCAATATCCAGATGATGATGATGATGATGATGATGATGATGATGAT 341
DB 61 SerLeuAlaThrSerIleSerGlnMetValLysThrGlnGlyLysGlyAlaLysArgLys 80
QY 342 ACCCTCGAGGAGAGAGAAATGCGAGTGAAGAGCTTGAGAAAGAAAGTTTGTAAAGCC 401
DB 81 ThrSerGlnGlnGlnLysAspGlySerGlnGlnLysValGlnLysValCysLysAla 100
QY 402 TCTTGGGATCTTGTGCTGAGAGGCTATGCGCTGAGCGGAGGATGAGAGGAGAG 461
DB 101 SerSerValIlePheGlyLeuLysGlyTyrValAlaGlnLysGlnGlyLysGlnGly 120
QY 462 ATCGAGATGCCACGTCATCTGAGACGATCAACGAGAGATGAGGCCCCCATGCTCC 521
DB 121 MetGlnAspAlaIleValIleLeuAspAspIleThrGlnGlnLysCysArgProProSer 140
QY 522 CTCATTACTCGGCTTCATATTTTGTCTTTTGTGATGACATGAGAAATTCAGACCTCA 581
DB 141 LeuIleThrArgValSerTyrPheAlaValPheAspGlyLysGlyLysIleArgAlaSer 160
QY 582 AAATTTGCTGCAAGAAATTTGCATCAAACTTAATPAGAAATTTCTTAAGAGATGTA 641
DB 161 LysPheAlaAlaGlnAsnLeuIleGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
QY 642 ATCAGTGTAGAGAAACGCTGAGAGATGCTTTTGAACATTTCAAGCATACTGATGAA 701
DB 181 IleSerValGlnLysThrValLysArgCysLeuLeuAspThrPheLysIleThrAspGly 200
QY 702 GAGTTCCTTAACAGCTTCCAGCGAGAGGCTGCTGAGAAAGATGGGTCCATGCCACG 761
DB 201 GluPheLeuLysGlnIleSerSerGlnLysPheProAlaThrLysAspGlySerThrAlaThr 220
QY 762 TGTGTTGCTGCTGAGACAACTTTTATATTGCGAAGCTGCGAGATPAGTCGGGCAATC 821
DB 221 CysValLeuAlaValAspAsnIleLeuLysIleAlaIleAsnLeuGlyAspSerArgAlaIle 240
QY 822 TTGTGCTGTTATATAGAGAGATGCAAAAATGCGACCTTAAAGCTCAAGCAAGACAT 881
DB 241 LeuLysArgTyrAsnGlnLysSerGlnLysIleAlaIleAsnLeuSerLeuSerLysGlnIle 260
QY 882 AATCCAACTCAGTATGAGAGCGAGTGAAGATACAGAGGCTGAGAGAAAGCTCAAGGAT 941
DB 261 AsnProThrGlnTyrGlnGlnLysGlnLysGlnLysGlnLysGlnLysGlnLysGlnLys 280
QY 942 GGGCGTGTCTTGGCGCTGCTAGAGGCTGTCAGCTCCATTGGGAGCGGCGAGTCAAGCCG 1001
DB 281 GlyArgValLeuGlyValLeuGlnLysSerIleGlyAspGlyGlnLysLysArg 300
QY 1002 TGGCGTGTCACTCTGCGCCGACATCAGACGCTGACAGTCAACCCCAATGACAGGTTTC 1061
DB 301 CysGlyValIleThrSerValProAspIleArgArgCysGlnLeuThrProAspArgPhe 320
QY 1062 ATTTTGTGGCTGTGATGGGCTTTTCAAGGCTTTTCAACCCCAAGAGAACCGTGAATTC 1121
DB 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheThrProGlnLysAlaValAsnPhe 340

QY 1122 ATCTTGTCTGTCTGAGATGAAAAATCAGACCCGAGAGGAAAGTCCGAGCCGAC 1181
DB 341 IleLeuSerCysLeuGlnLysGlnLysIleGlnThrArgGlnGlyLysSerAlaAlaAsp 360
QY 1182 GCCCGCTAGAGACGCGCTGCAACAGCGCTGGCCCAAGAGCGGTGACCGCGGCTCGGCC 1241
DB 361 AlaArgTyrGlnAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgLysSerAla 380
QY 1242 GACAACTCAGTGTGATGTTGTGCGGATGAGGAC 1277
DB 381 AspAsnValThrValMetValValArgIleGlyHis 392
RESULT 8
US-09-612-473-2
/ Sequence 2, Application US/09612473
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Corley, Neil C.
/ APPLICANT: Guejler, Karl J.
/ APPLICANT: Shah, Purvi
/ TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
/ FILE REFERENCE: PF-0470-1 CIP
/ CURRENT APPLICATION NUMBER: US/09/612,473
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 09/013,881
/ NUMBER OF SEQ ID NOS: 55
/ SOFTWARE: PERL Program
/ SEQ ID NO 2
/ LENGTH: 392.
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incey ID No: 195647
US-09-612-473-2
Alignment Scores:
Pred. No.: 3,53e-156 Length: 392
Score: 2018.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.83% Indels: 0
Gaps: 0
US-09-935-124A-1 (1-1422) x US-09-612-473-2 (1-392)
QY 102 ATGGAACCTTTCGGGAGACCTGCGGAGCCCGCTGCGCGCGCGCGCGGAA 161
DB 1 MetAspLeuPheGlyAspLeuProGluPheGlySerProAlaAspGlyAsp 20
QY 162 GAAGCTCAGAAAGAACCCCTGCTCTTTGATGATCTCCACCCGCTGACAGTGGCATTCAGGT 221
DB 21 GluAlaGlnLysGlyProLeuLeuPheAspLeuProProAlaSerSerThrAspSer 40
QY 222 GGATCAGGGGACCTTGTCTTTTGTGATGATCTCCACCCGCTGACAGTGGCATTCAGGT 281
DB 41 GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerSerGlyAspSerGly 60
QY 282 TCTCTGGCCACATCAATATCCAGATGATGATGATGATGATGATGATGATGATGATGAT 341
DB 61 SerLeuAlaThrSerIleSerGlnMetValLysThrGlnGlyLysGlyAlaLysArgLys 80
QY 342 ACCCTCGAGGAGAGAGAAATGCGAGTGAAGAGCTTGAGAAAGAAAGTTTGTAAAGCC 401
DB 81 ThrSerGlnGlnGlnLysAspGlySerGlnGlnLysValGlnLysValCysLysAla 100
QY 402 TCTTGGGATCTTGTGCTGAGAGGCTATGCGCTGAGCGGAGGATGAGAGGAGAG 461
DB 101 SerSerValIlePheGlyLeuLysGlyTyrValAlaGlnLysGlnGlyLysGlnGly 120

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Qy 462 ATGCAGATGCCCACTGATCTCTGAAAGACATCAGACCGAGAGTGAAGCCCATCTGCC 521
    |||
Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCysArgProPheSer 140
Qy 522 CTCATTAACCTGGGTTTCATATTTTGTCTTTTGTATGACATGACAGAAATTCAGAGCTCA 581
    |||
Db 141 LeuIleThrArgValSerTyrPheAlaValPheAspGlyHisGlyIleArgAlaSer 160
Qy 582 AAATTTGTCACAGAAATTTGATCAAAAATTAAATGAGAAATTTCTTAAGAGATGTA 641
    |||
Db 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
Qy 642 ATCAGCTGTAGAGAAACCGTGAAGAATGCTTTTGGACATTTTCAAGCATCTGATGAA 701
    |||
Db 181 IleserValGluLysThrValLysArgCysLeuLeuAspThrPheLysHisThrAspGlu 200
Qy 702 GAGTTCCTTAAACAAGCTTCCAGCGAGAGCCGCTGGAAAGATGGGTCCATGCCAG 761
    |||
Db 201 GluPheLeuLysGlnAlaSerSerGlnLysProAlaTrpLysAspGlySerThrAlaThr 220
Qy 762 TGTGTTCTGCTGTAGAACAACTTTTATATTCGCAACCTCGAGATGATGCGGCAATC 821
    |||
Db 221 CysValLeuAlaValAlaSerAsnIleLeuTyrIleAlaAsnLeuGlyAspSerArgAlaIle 240
Qy 822 TTGTGCTGTATATAGAGAGACTCAAAAACATGCAGCTTAAAGCTTCAGCAAAAGCAT 881
    |||
Db 241 LeuCysArgTyrAsnGluGlnSerGlnLysHisAlaAlaLeuSerLeuSerLysGlnHis 260
Qy 882 AATCCAACTCAGATGAAGAAGCGAGATGAGATGACAGAGCTGGAGAAACGTCAGGGAT 941
    |||
Db 261 AsnProThrGlnTyrGlnGluAsnMetArgIleGlnLysAlaGlyIleAsnValAlaArgAsp 280
Qy 942 GGGCGTGTGTTGGCGCTGTAGAGGTGTCAAGCTCCATTTGGGAGCGGAGATCAAGCCG 1001
    |||
Db 281 GlyArgValLeuGluValIleuGluValSerArgSerIleGlyAspGlyGlnTyrLysArg 300
Qy 1002 TGGGTGTCACTCTGTGCCGACATCAAGCTGTCAGCTGACCCCAATGACAGTTTC 1061
    |||
Db 301 CysGlyValIleThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
Qy 1062 ATTTTGTGGCGTGNATGGGCTTCAGAGTCTTTATCCCGAAGAACCGTGAACCTTC 1121
    |||
Db 321 IleLeuLeuAlaCysAsnArgLysLeuPheLysValPheThrProGluGluAlaValAsnPhe 340
Qy 1122 ATCTTGTCTGTCTCGAGATGAAAGATCCAGACCGGGAAGGAAGTCCGACGCCGAC 1181
    |||
Db 341 IleLeuSerCysLeuGlnAspGluLysIleGlnThrArgGluGlyLysSerAlaAlaAsp 360
Qy 1182 GCCCGCTACGAAGACCTTCGCAACAGGCTGGCCACAGAGCGGTGACGGGGCTCGGCC 1241
    |||
Db 361 AlaArgTyrGluAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgGlySerAla 380
Qy 1242 GACAAGTCATCTGATGTGTGGTGGTGGATGAGGCAC 1277
    |||
Db 381 AsnAsnValThrValMetValValArgIleGlyHis 392

RESULT 9
US-09-724-730-2
; Sequence 2: Application US/09724730
; GENERAL INFORMATION:
; APPLICANT: Hannigan, Gregory E.
; TITLE OF INVENTION: Novel Protein Phosphatase and Methods of
; FILE REFERENCE: KINE-016
; CURRENT APPLICATION NUMBER: US/09/724,730
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,225
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-724-730-2

Alignment Scores:
Pred. No.: 3,536-156 Length: 392
Score: 2018.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.83% Indels: 0
DB: 21 Gaps: 0

US-09-935-124a-1 (1-1422) x US-09-724-730-2 (1-392)

Qy 102 ATGACCTCTTCGGGAGACTGCGGAGCCGAGCGCTGCGCGCCGCTGCGCGGAAA 161
    |||
Db 1 MetAspLeuPheGlyAspLeuProGluArgSerProAlaSerProAlaAlaGlyLys 20
Qy 162 GAGCTCAGAAAGACCCCTGCTCTTATGATGACCTCCGCGCCAGCATGACTCA 221
    |||
Db 21 GlnAlaGlnLysGlyProLeuLeuPheAspLeuProProAlaSerThrAspSer 40
Qy 222 GAGTACAGGGGGACCTTGTCTTTTGTATGATCTCCACCGCTAGCAGTGGCATTCAGGT 281
    |||
Db 41 GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerSerGlyAspSerGly 60
Qy 282 TCTCTTGCACATCAATATCCAGATGTTAAAGACTGAAGGGAAGAGCAAGAGAAA 341
    |||
Db 61 SerLeuAlaThrSerIleSerGlnMetValLysThrGluGlyLysGlyAlaLysArgLys 80
Qy 342 ACCTCCAGAGAAAGAGAAATGGCAGTGAAGACTTTGTGGAAGAAAGAAAGTTGTTAAAGCC 401
    |||
Db 81 ThrSerGluGluGluGlyLysAsnGlySerGluGluLeuValGluLysLysValCysLysAla 100
Qy 402 TCTTGGATGATCTTTGCTGAAGGGCTATGTGCTGAGCGGAGAGGAGAGGAGG 461
    |||
Db 101 SerSerValIlePheGlyLeuLysGlyTyrValAlaGluLysGlyLysGluGluGlu 120
Qy 462 ATGCAGATGCCACGTATCTGTAACGACATCACCGAGAGTGTAGCCCCCATCTGCC 521
    |||
Db 121 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCysArgProPheSer 140
Qy 522 CTCATTAACCTGGGTTTCATATTTTGTCTTTTGTATGACATGACAGAAATTCAGAGCTCA 581
    |||
Db 141 LeuIleThrArgValSerTyrPheAlaValPheAspGlyHisGlyIleArgAlaSer 160
Qy 582 AAATTTGTCACAGAAATTTGATCAAAAATTAAATGAGAAATTTCTTAAGAGATGTA 641
    |||
Db 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
Qy 642 ATCAGCTGTAGAGAAACCGTGAAGAATGCTTTTGGACATTTTCAAGCATCTGATGAA 701
    |||
Db 181 IleserValGluLysThrValLysArgCysLeuLeuAspThrPheLysHisThrAspGlu 200
Qy 702 GAGTTCCTTAAACAAGCTTCCAGCGAGAGCCGCTGGAAAGATGGGTCCATGCCAG 761
    |||
Db 201 GluPheLeuLysGlnAlaSerSerGlnLysProAlaTrpLysAspGlySerThrAlaThr 220
Qy 762 TGTGTTCTGCTGTAGAACAACTTTTATATTCGCAACCTCGAGATGATGCGGCAATC 821
    |||
Db 221 CysValLeuAlaValAlaSerAsnIleLeuTyrIleAlaAsnLeuGlyAspSerArgAlaIle 240
Qy 822 TTGTGCTGTATATAGAGAGACTCAAAAACATGCAGCTTAAAGCTTCAGCAAAAGCAT 881
    |||
Db 241 LeuCysArgTyrAsnGluGlnSerGlnLysHisAlaAlaLeuSerLeuSerLysGlnHis 260
Qy 882 AATCCAACTCAGATGAAGAAGCGAGATGAGATGACAGAGCTGGAGAAACGTCAGGGAT 941
    |||
Db 261 AsnProThrGlnTyrGluGluAsnMetArgIleGlnLysAlaGlyLysValAlaArgAsp 280
Qy 942 GGGCGTGTGTTGGCGCTGTAGAGGTGTCAAGCTCCATTTGGGAGCGGAGATCAAGCCG 1001
    |||
Db 281 GlyArgValLeuGlyValLeuGluValSerArgSerIleGlyAspGlyGlnTyrLysArg 300
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! SEQ ID NO 2
! LENGTH: 392
! TYPE: PRT
! ORGANISM: Homo sapiens
US-09-935-124A-2

Alignment Scores:
Pred. No.: 3,53e-156 Length: 392
Score: 2018.00 Matches: 392
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 78.83% Indels: 0
DB: 23 Gaps: 0

US-09-935-124A-1 (1-1422) x US-09-935-124A-2 (1-392)

QY 102 ATGACCTCTTCGGGGAGCTCGCGGAGCCGCGGCGCGCCGGCTCGCGGGAAA 161
DB 1 MetaphleuphleglyAspLeuProGluArgSerProAlaIleGlyAs 20

QY 162 GAAGCTCAGAAAGAGACCCCTGCTTTGATGACCTCCCGCGGAGAGTACTGACTCA 221
DB 21 GluIleGlnlyGlyProLeuLeuPheAspLeuProAlaSerSerThrAspSer 40

QY 222 GATCAGAGGGGACCTTGGCTTTTATGATCTCCACCCGCTAGCAGTGGCATTGAGGT 281
DB 41 GlySerGlyGlyProLeuLeuPheAspLeuProAlaSerSerGlyAspSerGly 60

QY 282 TCTCTGGCACATCAATATCCAGATGGTAAAGACTGAAAGGAAAGGACAAAGAA 341
DB 61 SerLeuAlaThrSerIleSerGlnMetVallyStrnGlnlyLysGlyAlaLysArgLys 80

QY 342 ACCCTCGAGAGAGAGAGAAATGGCAGTGAAGACTTGTGAAAAGAAATTGTTAAAGCC 401
DB 81 ThrSerGlnGlnGlnLysAsnGlySerGlnLysValGlnLysValCysLysAla 100

QY 402 TCTTCGGTGAATCTTTGGTCTGAAGGCTATGTGCTGACCGGAGAGGTAGAGGAGAG 461
DB 101 SerSerValIlePheGlyLeuLysGlyLysValAlaGlnArgLysGlyGlnArgGlnGln 120

QY 462 ATGACGATGGCCAGTATCTCTGAACGACATCACGAGAGATGAGCCCATCTGCC 521
DB 121 MetGlnAspAlaHisValIleLeuAsnAspIleTrnGlnGlnCysArgProProSerSer 140

QY 522 CTCATTACTCGGGTTTCATATTTCTGTTTGTGATGACATGAGAAATTCGACCTCA 581
DB 141 LeuIleThrArgValSerThrPheAlaValPheAspGlnHisGlyGlyIleArgLysAspSer 160

QY 582 AAATTGGTCACAGAAATTTGCATCAAACTTAATCAGAAAATTTCTTAAGAGATGTA 641
DB 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyLysPVal 180

QY 642 ATCAGTGAAGAAAACGTGAAGAGATGCTTTTGGACACTTCAAGATCTGATGAA 701
DB 181 IleSerValGlnLysThrValLysArgCysLeuLeuAspTrnPheLysHisThrAspGln 200

QY 702 GAGTTCTTTAAACAAGCTTCCAGCAGAGCCTGCTGGAAGATGGGTCCACTGCCACG 761
DB 201 GluPheLeuLysGlnAlaSerSerGlnLysProAlaTrpLysAspGlySerThrLysThr 220

QY 762 TGTGTTCTGGCTGATGACAACTTTTATATTTGCCAACTTCGAGATGATGGGCAATC 821
DB 221 CysValIleuAlaValAspAsnIleLeuLysTrIleAlaAsnLeuGlyAspSerArgLysIle 240

QY 822 TTGCTCTCTTAATTAAGAGAGAGTCAAAAACATGACCTTAAAGCTTCAGCAAAGAGAT 881
DB 241 LeuCysArglyArgGlnGlnLysSerGlnLysAlaAlaLeuSerLeuSerLysGlnLys 260

QY 882 AATCCAACTCAGTATGAGAGCGAGTGAAGATACAGAAAGCTGAGAGAAACGTGAGGAT 941
DB 261 AsnProThrGlnTrnGlnGlnArgMetArgIleGlnLysAlaGlyGlyLysAsnValArgAsp 280

QY 942 GGGCGTGTGGGGCGTCTAGAGGTGTCACGCTCATTTGGGAGCGGCAAGTACAAGCGC 1001
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DB 281 GlyArgValLeuGlyValLeuGlnValSerArgSerIleGlyAspGlyGlnTrnLysArg 300

QY 1002 TGGCGTGCACCTCTGTGTCGCCGACATCAGACGCTGCAGTACCCCAATGACAGTTTC 1061
DB 301 CysGlyValIleThrSerValProAspIleArgArgCysGlnLeuTrnProAsnAspArgPhe 320

QY 1062 ATTTTGTGGCTGTGATGGGCTCTTCAAGGTCTTTTACCCGAGAAAGACCGTGAATTC 1121
DB 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheTrnProGlnGlnAlaValAsnPhe 340

QY 1122 ATCTTGTCTGTCTTCGAGAGATGAAAAGATCCAGACCCGGGAAAGGAATCCCGCAGCCAC 1181
DB 341 IleLeuSerCysLeuGlnAspGlnLysIleGlnTrnArgGlnGlyLysSerValAlaAsp 360

QY 1182 GCGCGCTACAGAGCGCTGCAACAGCGCTGCGCAACAGAGCGGTGACAGGAGCTCGAGCC 1241
DB 361 AlaArglyTrGlnAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgGlySerAla 380

QY 1242 GACAACGTCACTGTGATGATGGTGTGGGATAGGCGCAC 1277
DB 381 AspAsnValThrValMetValValArgIleGlyHis 392

RESULT 12
US-09-629-469A-10816
! Sequence 10816, Application US/09629469A
! GENERAL INFORMATION:
! APPLICANT: OTA, TOSHIO
! APPLICANT: ISOGAI, TAKAO
! APPLICANT: NISHIKAWA, TETSUO
! APPLICANT: HAYASHI, KOJI
! APPLICANT: SAITO, KAORU
! APPLICANT: YAMAMOTO, JUNICHI
! APPLICANT: ISHII, SHIZUKO
! APPLICANT: SUGIYAMA, TOMOYASU
! APPLICANT: KAKAMATSU, AI
! APPLICANT: NAGAI, KEIICHI
! APPLICANT: OTSUKI, TETSUJI
! TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
! FILE REFERENCE: 084335/0123
! CURRENT APPLICATION NUMBER: US/09/629, 469A
! CURRENT FILING DATE: 2000-07-28
! PRIOR APPLICATION NUMBER: JP 1999-248036
! PRIOR FILING DATE: 1999-07-29
! PRIOR APPLICATION NUMBER: JP 1999-300253
! PRIOR FILING DATE: 1999-08-27
! PRIOR APPLICATION NUMBER: JP 2000-118776
! PRIOR FILING DATE: 2000-01-11
! PRIOR APPLICATION NUMBER: JP 2000-183767
! PRIOR FILING DATE: 2000-05-02
! PRIOR APPLICATION NUMBER: JP 2000-241899
! PRIOR FILING DATE: 2000-06-09
! PRIOR APPLICATION NUMBER: 60/159,590
! PRIOR FILING DATE: 1999-10-18
! PRIOR APPLICATION NUMBER: 60/183,322
! NUMBER OF SEQ ID NOS: 19025
! SOFTWARE: PatentIn Ver. 2.1
! SEQ ID NO 10816
! LENGTH: 392
! TYPE: PRT
! ORGANISM: Homo sapiens
US-09-629-469A-10816

Alignment Scores:
Pred. No.: 6,21e-156 Length: 392
Score: 2015.00 Matches: 391
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.74% Mismatches: 0
Query Match: 78.71% Indels: 0
DB: 20 Gaps: 0

US-09-935-124A-1 (1-1422) x US-09-629-469A-10816 (1-392)
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QY 102 ATGACCTCTTCGGGGACCTGCGGAGCCGAGGGCTGCGGGCCGGCTGCGGGAAA 161
 DB 1 MetAspLeuPheGlyAspLeuProGluuArgSerProAlaIleGlyLys 20
 QY 162 GAAGCTCAGAAAGAACCCCTGCTTTGATGACCTCCCTCGGCGAGGTGACTGACCA 221
 DB 21 GluAlaGlnuysGlyProLeuLeuPheAspLeuProProAlaSerSerThrAspSer 40
 QY 222 GGATCAGGGGAGACCTTGTCTTTGATGATCTCCACCCGCTAGCGATGCGCATTCAGGT 281
 DB 41 GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerSerGlyAspSerGly 60
 QY 282 TCTCTTCCACATCATATATCCAGATGCTAAAGACTGAAAGGAAAGCAAGCAAAA 341
 DB 61 SerLeuAlaThrSerMetSerGlnMetValuysThrGluGluGlySerGlyAlaValysArgLys 80
 QY 342 ACCCTCCGAGAAAGAAAGATGCGAGTGAAGAGCTTGTGAAAAGAAAGTTTGTAAAGCC 401
 DB 81 ThrSerGluGluGluuysaenGlySerGluGluLeuValuysLysValuysValuysAla 100
 QY 402 TCTTGCTGATCTTTGCTGAGAGGGGCTATGCTGAGCGGAGCGGAGGAGGAGAG 461
 DB 101 SerSerValuysIlePheGlyLeuLysGlyTyrValuysAlaGluArgGlySerGlyuArgGlu 120
 QY 462 ATGACAGATGCCCACTGATACCTGAAAGCAATCCAGAGAGTGAAGGCCCATGCTCC 521
 DB 121 MetGlnAspAlaHisValuysIleLeuAsnAspIleThrGluGluGlySerArgProProSerSer 140
 QY 522 CTCATTACTGGGCTTCAATTTGCTGCTTTTGAAGCAATGAGAGAAATTCGAGCCCTCA 581
 DB 141 LeuIleThrArgValSerTyrPheAlaValuysPheAspGlyHisGlyIleHisGlyAlaSer 160
 QY 582 AAATTTGCTGCAAGAAATTTGCATCAAACTTAATCAAGAAATTTCTTAAGAGATGTA 641
 DB 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
 QY 642 ATCAGTGTAGAGAAACCGTGAAGAGATGCCCTTTGAGACCTTCAAGCATCTGATGAA 701
 DB 181 IleSerValuysGluysThrValuysLysArgCysLeuLeuAspThrPheValuysHisIleThrAspGly 200
 QY 702 GAGTTCCTTAAACAAGCTTCCAGCGCAGAGGCTGCTGGAAGAGATGGGTCCAGCTCCAG 761
 DB 201 GluPheLeuLysGlnAlaSerSerGlnLysSerProAlaIleArgLysAspGlySerThrAlaThr 220
 QY 762 TGTGCTGCTGTAGCAAACTTCTTAATTTGCCCAAGCTCGAGATGTCGGGCAATC 821
 DB 221 CysValuysLeuAlaValuysAsnIleLeuLysIleHisAlaAsnLeuGlyAspSerArgAlaIle 240
 QY 822 TTGTGCTTATATGAGAGAGTCAAAAGATGACGCTTAAGCTTCAAGCAAGAGCAT 881
 DB 241 LeuCysArgTyrAsnGlnuysGlnuysSerGlnuysHisAlaIleuysSerLeuysSerLysGluHis 260
 QY 882 AATCCAATCAGTATGAGAGCGGATGAGATACAGAAAGCTGAGAGAAAGCTCAGGGAT 941
 DB 261 AsnProThrGlnuysArgGlnuysMetArgIleGlnuysAlaGlyIleAsnValuysAsp 280
 QY 942 GGGCGTGTGTCGCGCTGTAAGAGTGTCAAGCTTCATTGGGGAACGGGCAATCAAGCC 1001
 DB 281 GlyArgValuysLeuGlyValuysLeuGluValuysSerArgSerIleGlyAspIleGlnuysArg 300
 QY 1002 TGGCGTGTCACTCTGTGCCGACATCAAGAGCTGCCAGCTGACCCCAATGACAGTTTC 1061
 DB 301 CysGlyValuysThrSerValuysProAspIleArgArgCysGlnuysLeuThrProAsnAspArgPhe 320
 QY 1062 ATTTGTTGGCTGTGATGGGCTCTTCAAGGTCTTAAACCCAGAAAGACCGTGAATTC 1121
 DB 321 IleLeuLeuAlaCysAspGlyLeuPheLysValuysPheThrProGluGluAlaValuysAsn 340
 QY 1122 ATCTTGTCTGTCTCGAGATGAAGATCCAGACCCGAGAGAGGAGATCCGACCGAC 1181
 DB 341 IleLeuSerCysLeuGluAspGluysIleGlnuysThrArgGluGluLysSerAlaIleAsp 360

QY 1182 GCCGCTACAGAGACCTGCAACAGGCTGGCCCAAGAGCGGTGAGCGGGGCTCGGCC 1241
 DB 361 AlaArgTyrGluAlaIleCysAsnArgLeuAlaAsnValuysAlaGlnArgGlySerAla 380
 QY 1242 GACAAGCTCACTGTGATGGTGTGTCGAGATGAGGAC 1277
 DB 381 AspAsnValuysThrValuysMetValuysAlaArgIleGlyHis 392
 RESULT 13
 US-09-488-725A-1914
 ; Sequence 1914, Application US/09488725A
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq Inc
 ; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
 ; FILE REFERENCE: 784PCT
 ; CURRENT FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US/09/488,725
 ; PRIOR FILING DATE: 2000-01-21
 ; PRIOR APPLICATION NUMBER: US09/552,317
 ; PRIOR FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: US09/598,042
 ; PRIOR FILING DATE: 2000-06-20
 ; PRIOR APPLICATION NUMBER: US09/620,312
 ; PRIOR FILING DATE: 2000-07-19
 ; PRIOR APPLICATION NUMBER: US09/653,450
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: US09/662,191
 ; PRIOR FILING DATE: 2000-09-14
 ; PRIOR APPLICATION NUMBER: US09/693,036
 ; PRIOR FILING DATE: 2000-10-19
 ; PRIOR APPLICATION NUMBER: US09/727,344
 ; PRIOR FILING DATE: 2000-11-29
 ; NUMBER OF SEQ ID NOS: 7144
 ; SOFTWARE: pc_FL_genes_b Versions 1.0
 ; SEQ ID NO 1914
 ; LENGTH: 392
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-488-725A-1914
 Alignment Scores:
 Pred. No.: 756-156 Length: 392
 Score: 2014.00 Matches: 391
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.74% Mismatches: 0
 Query Match: 78.67% Indels: 0
 DB: Gaps: 0
 US-09-935-124A-1 (1-1422) x US-09-488-725A-1914 (1-392)
 QY 102 ATGACCTCTTCGGGGACCTGCGGAGCCGAGGGCTGCGGGCCGGCTGCGGGAAA 161
 DB 1 MetAspLeuPheGlyAspLeuProGluuArgSerProAlaIleGlyLys 20
 QY 162 GAAGCTCAGAAAGAACCCCTGCTTTGATGACCTCCCTCGGCGAGGTGACTGACCA 221
 DB 21 GluAlaGlnuysGlyProLeuLeuPheAspLeuProProAlaSerSerThrAspSer 40
 QY 222 GGATCAGGGGAGACCTTGTCTTTGATGATCTCCACCCGCTAGCGATGCGCATTCAGGT 281
 DB 41 GlySerGlyGlyProLeuLeuPheAspLeuProProAlaSerSerGlyAspSerGly 60
 QY 282 TCTCTTCCACATCATATATCCAGATGCTAAAGACTGAAAGGAAAGCAAGCAAAA 341
 DB 61 SerLeuAlaThrSerMetSerGlnMetValuysThrGluGluGlySerGlyAlaValysArgLys 80
 QY 342 ACCCTCCGAGAAAGAAAGATGCGAGTGAAGAGCTTGTGAAAAGAAAGTTTGTAAAGCC 401
 DB 81 ThrSerGluGluGluuysaenGlySerGluGluLeuValuysLysValuysValuysAla 100
 QY 402 TCTTGCTGATCTTTGCTGAGAGGGGCTATGCTGAGCGGAGGAGGAGAG 461


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Db 101 SerSerValIIEpHeGlyLeuLySeGlyTyValAlaGlnArgLySeGlyGlnArgGlnGln 120
Qy 462 ATGCAGATGCCACGTCATCTCTGAACGACATCACCGAGAGTGAAGCCCATCGTCC 521
Db 121 MetGlnAspAlaHISValIIEleuMenAspIIEthGlnGlnCysArgProProSerSer 140
Qy 522 CTCATTACTCGGGGTTTCATATTTTGTGTTTGTATGACATGAGAGAAATCGAGCTCA 581
Db 141 LeuIIEthArgValSerTyRpheAlaValIIPheAspGlyHISGlyGlyIIEthArgAlaSer 160
Qy 582 AAATTGCTGCACAGAAATTTGATCAAAACTTAATCAGAAATTTCTTAAGAGAGATGA 641
Db 161 LysPheAlaAlaGlnAsnLeuHISGlnAsnLeuIIEArgLysPheProLysGlyAspVal 180
Qy 642 ATCAGTGTAGAGAAAACCGTAAGAGATGCTTTTGGACACTTTCAGACTCTAGTAA 701
Db 181 IIESerValGlnLysEthrValIIEAspGlySeLeuLeuAspThrPheLysHISethrAspGln 200
Qy 702 GAGTTCTTTAAACAAGCTTCCAGCCGAAAGCTGCTGGAAGATGGGTCCACTGCGCAG 761
Db 201 GlnPheLeuLyGlnAlaSerSerGlnLysProAlaTrpLysAspGlySerThrAlaThr 220
Qy 762 TGTGTTCTGCGCTGAGACAACATCTTTATATTTGCAACTCGGAGATGCGGGCAATC 821
Db 221 CysValIIEuAlaValAspAsnIIEuTyRIIEAlaAsnLeuGlyAspSerArgAlaIIE 240
Qy 822 TTGTCGCTTATATAGAGAGAGATCAAAAACATGACGCTTAAGCTTCAGCAAAAGACAT 881
Db 241 LeuCybArgTyRAsnGlnGlnSerGlnLysHISAlaAlaIIEuSerIIEuSerLySeGlnHIS 260
Qy 882 AATCCAACTCAGTATGAGAGCGGATGAGATACAGAAAGCTGAGAGAAAGCTCAGGAT 941
Db 261 AsnProthGlnTyArgGlnArgMetArgIIEGlnLysAlaGlyLysAsnValIIEArgAsp 280
Qy 942 GGGCGGTGTTTGGGGGTGTAGAGGTCACGCTCCATTGGGGAGCGGGAGATCAAGCC 1001
Db 281 GlyArgValLeuGlyValIIEuGlnValSerArgSerIIEGlyAspGlyGlnTyRAspArg 300
Qy 1002 TGGCGTGTACCTCTGTGCGCCGACATCAGACGCTGCGACGCTCAACCCCAATGACAGTTC 1061
Db 301 CysGlyValIIEthSerValIIEProAspIIEArgArgCybGlnIIEthProAsnAspArgPhe 320
Qy 1062 ATTTGTTGGCTGTGTGAGGGGCTTTCAAGGCTTTTACCCGAGAAAGCCGTGAATCTTC 1121
Db 321 IIEleuLeuAlaCybAspGlyLeuPheLysValIIEthProGlnGlnAlaValIIEAspHe 340
Qy 1122 ATCTTGTCTCTGTGAGATGAAAGATCCAGACCCGGGAGGGAATGCCGACCGCAC 1181
Db 341 IIEleuSerCybLeuGlnAspGlnLysIIEGlnThrArgGlnGlyLysSerAlaAlaGln 360
Qy 1182 GCGCCGCTACGAAGACGCTGCAACAGCGTGGCCCAACAGCGGCTGCAAGCGGCTCGGCC 1241
Db 361 AlaArgTyRglnAlaAlaIIECybAsnArgLeuAlaAsnLysAlaValGlnArgGlySerAla 380
Qy 1242 GACAACTGCTAGTGTGTGTGCGGATGAGGCGAC 1277
Db 381 AsnAsnValIIEthValIIEMetValIIEArgIIEGlnHIS 392

RESULT 14
US-09-791-537-49417
; Sequence 49417, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 49417
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; LENGTH: 392
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-791-537-49417

Alignment Scores:
Pred. No.: 4,79e-149 Length: 392
Score: 1931.00 Matches: 373
Percent Similarity: 96.94% Conservative: 7
Best Local Similarity: 95.15% Mismatches: 12
Query Match: 75.43% Indels: 0
DB: 21 Gaps: 0

US-09-935-124A-1 (1-1422) x US-09-791-537-49417 (1-392)
Qy 102 ATGCAGCTCTTCGGGGACCTGCGGAGCCGAGCGCTGCGCGGCGCGGCTGCGGGAAA 161
Db 1 MetAspLeuPheGlyAspLeuProGlnProGlnArgProProArgProSerAlaGlyLys 20
Qy 162 GAACTCAGAAAGAACCCCTGCTTTGATGACCTCCCTCGGCGCAGAGATGACTCA 221
Db 21 GlnAlaGlnGlnGlyProValIIEuPheGlnAspLeuProProthSerSerThrAspSer 40
Qy 222 GGAATCAGGGGAACTTTCCTTTTGTATGATCTCCACCCGCTGACAGTGGCGATTCAGGT 281
Db 41 GlySerGlyGlyProLeuLeuPheAspGlyLeuProProAlaGlySerGlyAsnSerGly 60
Qy 282 TCTCTGCGACATCAATATCCAGATGGTAAAGACTGAAGGGAAGAGCAAGAGAAA 341
Db 61 SerLeuAlaIIEthSerGlySerGlnValIIEuLysAsnGlnGlyLysGlyAlaLysArgLys 80
Qy 342 ACCCTCGAGAAAGAGAAATGCGACAGTGAAGGCTTGTGAAAGAAAGTTTGTAAAGCC 401
Db 81 AlaProGlnGlnGlnLysAsnGlyGlyGlyGlnLeuValGlnLysLysValCysLysAla 100
Qy 402 TCTTGGTGATCTTTGGTCTGAAGGCTATGTGCTGACCGGAGGCTGAGAGGAGAG 461
Db 101 SerSerValIIEpHeGlyLeuLySeGlyTyValAlaGlnArgLySeGlyGlnArgGlnGln 120
Qy 462 ATGCAGATGCCACGTCATCTCTGAACGACATCACCGAGAGTGAAGCCCATCGTCC 521
Db 121 MetGlnAspAlaHISValIIEleuMenAspIIEthGlnGlnCysArgProProSerSer 140
Qy 522 CTCATTACTCGGGGTTTCATATTTTGTGTTTGTATGACATGAGAGAAATCGAGCTCA 581
Db 141 LeuIIEthArgValSerTyRpheAlaValIIPheAspGlyHISGlyGlyIIEthArgAlaSer 160
Qy 582 AAATTGCTGCACAGAAATTTGATCAAAACTTAATCAGAAATTTCTTAAGAGAGATGA 641
Db 161 LysPheAlaAlaGlnAsnLeuHISGlnAsnLeuIIEArgLysPheProLysGlyAspVal 180
Qy 642 ATCAGTGTAGAGAAAACCGTAAGAGATGCTTTTGGACACTTTCAGACTCTAGTAA 701
Db 181 IIESerValGlnLysEthrValIIEAspGlySeLeuLeuAspThrPheLysHISethrAspGln 200
Qy 702 GAGTTCTTTAAACAAGCTTCCAGCCGAAAGCTGCTGGAAGATGGGTCCACTGCGCAG 761
Db 201 GlnPheLeuLyGlnAlaSerSerGlnLysProAlaTrpLysAspGlySerThrAlaThr 220
Qy 762 TGTGTTCTGCGCTGAGACAACATCTTTATATTTGCAACTCGGAGATGCGGGCAATC 821
Db 221 CysValIIEuAlaValAspAsnIIEuTyRIIEAlaAsnLeuGlyAspSerArgAlaIIE 240
Qy 822 TTGTCGCTTATATAGAGAGAGATCAAAAACATGACGCTTAAGCTTCAGCAAAAGACAT 881
Db 241 LeuCybArgTyRAsnGlnGlnSerGlnLysHISAlaAlaIIEuSerIIEuSerLySeGlnHIS 260
Qy 882 AATCCAACTCAGTATGAGAGCGGATGAGATACAGAAAGCTGAGAGAAAGCTCAGGAT 941
Db 261 AsnProthGlnTyArgGlnArgMetArgIIEGlnLysAlaGlyLysAsnValIIEArgAsp 280
Qy 942 GGGCGGTGTTTGGGGGTGTAGAGGTCACGCTCCATTGGGGAGCGGGACAGTCAAGCGC 1001
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Db 281 GIAYGValleuglyValleuglyValsergserilleglyaspolygintyrylsarg 300
QY 1002 TCGGGTGCACCTGTGTGCCGACATCAGACCGCTGCCAGCTGACCCCAATGACAGGTTC 1061
Db 301 CysGlyValThrSerValProaspIleargArgCysGlnLeuThrProaspnsparghe 320
QY 1062 ATTTGTTGGCCTGTGATGGGCTCTTCAAGTCTTACCCGAGAGAGGCGGTGAATTC 1121
Db 321 IleuLeuAlaCysaspGlyLeuPheThrProGlnGlnAlaValasphe 340
QY 1122 ATCTGTCTGTCTCGAGATGAGAAAGATCCAGACCGGAGAGGAAAGTCCGACGCCAC 1181
Db 341 IleuSerCysleuGlnaspGlyValIleGlnThrArgGlnGlyValProAlaValasp 360
QY 1182 GCCCGTACAGACGAGCTGCAAGCTGCGCAAGGCGGTGACGCGGCTCGGC 1241
Db 361 AlaArgTyrGlnAlaAlaCysaspArgLeuAlaAsnValGlnAlaGlySerAla 380
QY 1242 GACAACTGCTGTGATGTGTGTGCGGATAGGCTC 1277
Db 381 AspAsnValThrValMetValAlaArgIleGlyHis 392
RESULT 15
PCT-US02-25455-22
Sequence 22, Application PC/TUS0225455
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATION OF DARPP-32 PHOSPHORYLATION
FILE REFERENCE: 11181-005
CURRENT APPLICATION NUMBER: PCT/US02/25455
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,641
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 392
TYPE: PRT
ORGANISM: Rattus sp.
PCT-US02-25455-22
Alignment Scores:
Pred. No: 1 026-148 Length: 392
Score: 1927.00 Matches: 372
Percent Similarity: 96.94% Conservative: 8
Best Local Similarity: 94.90% Mismatches: 12
Query Match: 75.27% Indels: 0
Gaps: 0
US-09-935-124A-1 (1-1422) x PCT-US02-25455-22 (1-392)
QY 102 ATGAGACCTCTTCCGGGACCTGCGGAGCCGAGCGCTGCGCGCTCGGCTGCCGAGAA 161
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QY 162 GAAGCTCAGAAAGAGACCCCTGCTCTTGTATGACCTCCCTCGGCGCAGAGTACTGACTCA 221
Db 21 GlnAlaGlnGlnGlyProValIleuPheGlnaspLeuProThrSerSerThrAspSer 40
QY 222 GAATCAGGGGGACCTTGTGCTTTTGTATGATCTCCACCGCTACGAGTGGCATTCAGT 281
Db 41 GlySerGlyGlyProLeuLeuPheaspGlyLeuProAlaGlySerIlyaspSerGly 60
QY 282 TCTCTTGCACATCATATATCCGAGTGTAAAGACTGAAGAGAAAGAGCAAGAGAAA 341
Db 61 SerLeuAlaThrSerGlySerGlnValValIlyaspGlnGlySerIlyAlaIlyArgHis 80
QY 342 ACCCTCCGAGAGAGAAAGAAATGCGGTGAGAGCTTGTGAGAAAGAAATTTGTAAAGCC 401
Db 81 AlaProGlnGlnGlnaspAsnGlyGlyGlnGlnLeuValGlnIlySerValCysIlyAla 100
QY 402 TCTTGGTGATCTTGTCTGAAGGGCTATGTGGCTAGCGGAGGAGGTAGAGGAGAG 461

Db 101 SerSerValIlePheGlyLeuPheGlyTyrValAlaGlnArgIlyGlnArgGlnGln 120
QY 462 ATGCAGATATGCCCAACGTCATCCGAGACGATCACCGAGAGAGGTGAGCCCAATCGTCC 521
Db 121 MetGlnaspAlaHisValIleLeuaspIleThrGlnGlnCysaspProProSer 140
QY 522 CTGATTAATCCGGTTCATATTTTGTGCTTTTGAATGAGCACTGAGAGAAATTCGAGCTCA 581
Db 141 LeuIleThrArgValSerTyrPheAlaValPheaspGlyHisGlyGlyIleArgAlaSer 160
QY 582 AAATTTGTCGACAGAAATTTGCTCAAACTTAATCAGAAATTTCCCTAAAGAGAGATGA 641
Db 161 LysPheAlaAlaGlnAsnLeuHisGlnAsnLeuIleArgIlySerProIlySerGlyaspVal 180
QY 642 ATCAGTGTAGAGAAACCGTGAAGAGATCCTTTTGAACATTTCAAGCATATGATGA 701
Db 181 IleSerValGlnIlyThrValIlyArgCysleuLeuAspThrPheIlyHisIlyAspGln 200
QY 702 GAGTTCCTTAAACAGCTTCACGACGAGAGCCTGCTGAAAGAGGCTCACTGCGACG 761
Db 201 GluPheLeuIlyGlnAlaSerSerGlnIlyProAlaIlyPlyaspGlySerThrAlaThr 220
QY 762 TGTGTCTGTGTGAGCAACATTTCTTATTTGCAACCTCGAGATGATGCGGCAATC 821
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QY 822 TTGTGTCTGTATATGAGAGAGATCAAAACATGACGCTTAAGCTTCAGCAAAAGCAT 881
Db 241 LeuCysArgTyrAsnGlnGlnIlySerGlnIlyHisAlaAlaLeuSerLeuSerIlyGlnHis 260
QY 882 AATCCAACTCATATGAGAGCGGATGAGAGATGACAGAGCGGTGAGAGAAAGTCAAGCAT 941
Db 261 AsnProGlnIlyArgIlyGlnArgMetArgIleGlnIlyAlaGlyIlyAsnValAlaArgAsp 280
QY 942 GGGCGGTGTTGGCGGTCTGTGAGTGTGACGCTCATTTGGGAGCGGCGAGTCAAGCCG 1001
Db 281 GIAYGValleuglyValleuglyValsergserilleglyaspolygintyrylsarg 300
QY 1002 TCGGGTGCACCTGTGTGCCGACATCAGACCGCTGCCAGCTGACCCCAATGACAGGTTC 1061
Db 301 CysGlyValThrSerValProaspIleargArgCysGlnLeuThrProaspnsparghe 320
QY 1062 ATTTGTTGGCCTGTGATGGGCTCTTCAAGTCTTACCCGAGAGAGGCGGTGAATTC 1121
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Db 341 IleuSerCysleuGlnaspGlyValIleGlnThrArgGlnGlyValProAlaValasp 360
QY 1182 GCCCGTACAGACGAGCTGCAAGCTGCGCAAGGCGGTGACGCGGCTCGGC 1241
Db 361 AlaArgTyrGlnAlaAlaCysaspArgLeuAlaAsnValGlnAlaGlySerAla 380
QY 1242 GACAACTGCTGTGATGTGTGTGCGGATAGGCTC 1277
Db 381 AspAsnValThrValMetValAlaArgIleGlyHis 392
RESULT 16
US-10-218-137-22
Sequence 22, Application US/10218137
GENERAL INFORMATION:
APPLICANT: Greengard, Paul
APPLICANT: Svenningsen, Per
APPLICANT: Rakhilin, Sergey
APPLICANT: Starikova, Natalia
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATION OF DARPP-32 PHOSPHORYLATION
FILE REFERENCE: 11181-005
CURRENT APPLICATION NUMBER: US/10/218,137
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 60/311,641
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 23

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-218-137-22

Alignment Scores:
Pred. No.: 1,02e-148      Length: 392
Score: 1927.00           Matches: 372
Percent Similarity: 96.94%      Conservative: 8
Best Local Similarity: 94.90%    Mismatches: 12
Query Match: 75.27%           Indels: 0
DB: 26                      Gaps: 0

US-09-935-124A-1 (1-1422) x US-10-218-137-22 (1-392)

Oy 102 ATGACACCTTTGGGGGACCTGCGGAGCCGCGGCGCGCGCGCGCGCGGAGAA 161
Db 1 MetAspLeuPheGlyAspLeuProGluProGluArgAlaProArgProSerAlaGlyLys 20
Oy 162 GAAGCTCAGAAAGAGACCCCTGCTTTGATGACCTCCCTCCGGCCAGAGTACTGACTCA 221
Db 21 GluAlaGlnGlnGlyProValLeuPheGluAspLeuProThrSerSerThrAspSer 40
Oy 222 GGATCAGGGGACCTTTGCTTTTGTATGATCTCCACCCGCTAGCAGTGCAGATTCAAGT 281
Db 41 GlySerGlyGlyProLeuLeuPheAspGlyLeuProProAlaGlySerGlyAsnSerGly 60
Oy 282 TCTCTTGGCCACATCATATCCCAAGTGTAAAGACTGAAGGAGAAAGACCAAGAGAAA 341
Db 61 SerLeuAlaThrSerGlySerGlnValValLysAsnGlnGlyLysGlyAlaLysArgLys 80
Oy 342 ACCTCCGAGAGAGAGAAAGATGGACACTGAAGACTGTGTAAGAAAGATTGTAAAGCC 401
Db 81 AlaProGlnGlnGlnLeuAsnGlnGlyGlnGlnLeuValGlnLysValCysLysAla 100
Oy 402 TCTTGGGTATCTTTGCTGTGAAGGGCTATGTGCTGACGAGGAGGTGAGAGAGAG 461
Db 101 SerSerValIlePheGlyLeuLysGlyTyrValAlaGluArgLysGlyLysArgGlnGln 120
Oy 462 ATGCAGAGATGCCACGCTCATCTGAAACGACATCACCGAGAGATGTAGCCCGCATGTCC 521
Db 121 MetGlnAspAlaIleValIleLeuAsnAspIleThrGlnGlnCysAsnProProSerSer 140
Oy 522 CTCATTAATCGGGATTTCATATTTTGTGTTTGTATGATGACATGAGAGAAATTGAGCCTCA 581
Db 141 LeuIleThrArgValSerTyrPheAlaValPheAspGlyHisGlyLysIleArgAlaSer 160
Oy 582 AAATTGCTGCACAGAAATTGCATCAAACTTAATCAGAAAATTTCTTAAGAGAGATGTA 641
Db 161 LysPheAlaIleAlaGlnAsnLeuHisGlnAsnLeuIleArgLysPheProLysGlyAspVal 180
Oy 642 ATCAGTGTGAGAAAACGCTGAAGAGATGCTTTTGGACATTTCAAGCATACTGATGAA 701
Db 181 IleSerValGlnLysThrValLysArgCysLeuLeuAspThrPheLysHisThrAspGln 200
Oy 702 GAGTTCCTTAAACAAGCTTCCAGCCAGAGCCGCTGAAAGATGGGTCCACTGCGCAAG 761
Db 201 GluPheLeuLysGlnIleAspSerGlnLysProAlaTyrLysAspLysSerThrAlaThr 220
Oy 762 TGTGTTCTGCTGTGACACAATCTTTTATTTGCAACCTCGAGATGTCGGGCAATC 821
Db 221 CysValIleLeuAlaValAspAsnIleLeuTyrIleAlaAsnLeuGlyAspSerThrAlaIle 240
Oy 822 TTGTGTCTGTTATATGAGAGAGTCAAAAACATGCAGCCTTAAGCCTTACGCAAAAGCAT 881
Db 241 LeuCysArgTyrAsnGlnGlnLysSerGlnLysHisAlaAlaLeuSerLeuSerLysGlnHis 260
Oy 882 AATCCAACTCAGATATGAAGAGGAGTGAAGATACGAAGGCTGAGAGAAACCTCAGGGAT 941
Db 261 AsnProThrGlnTyrGlnGlnLysArgMetArgIleGlnLysAlaGlyGlyAsnValAlaAsp 280
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Oy 942 GGGCGTGTTTTGGCGCTGTACAGGTGTACGCTTCATTTGGGGAGCGGAGTACAAGCGC 1001
Db 281 GlyArgValIleGlnGlyValLeuGlnValSerIleArgSerIleGlyAspGlyGlnTyrLysArg 300
Oy 1002 TGGCGGTGCACCTCTGTGTCGCCGACATCAGACGCTCCGAGCTGAGCCCAATGACAGTTC 1061
Db 301 CysGlyValIleThrSerValProAspIleArgArgCysGlnLeuThrProAsnAspArgPhe 320
Oy 1062 ATTTGTTGCGCTGTGATGGGCTCTTCAAGGTCTTTACCCGAGAAAGACCGGTGAATTC 1121
Db 321 IleLeuLeuAlaCysAspGlyLeuPheLysValPheThrProGlnGlnAlaValAsnPhe 340
Oy 1122 ATCTTGTCTCTGTCTGAGAGTGAAGAAATCCAGACCCGGGAAAGGAGTCCGACCCGAC 1181
Db 341 IleLeuSerCysLeuGlnLysAspGlnLysIleGlnThrArgGlnGlyLysProAlaValAsp 360
Oy 1182 GCCGCTACGAAGCAGCCTTCGACAAGCTGCGCCACAGCGCGTGCACCGGGCGCTCGGCC 1241
Db 361 AlaArgTyrGlnAlaAlaCysAsnArgLeuAlaAsnLysAlaValGlnArgGlySerAla 380
Oy 1242 GACAAGTCACTGTGATGGTGGTGGCGATAGGGCAC 1277
Db 381 AspAsnValThrValMetValValArgIleGlyHis 392

RESULT 17
US-60-245-228-374
; Sequence 374, Application US/60245228
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN CYCLASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN CYCLASE PROTEINS, AND USES
; FILE REFERENCE: C1000878
; CURRENT APPLICATION NUMBER: US/60/245,228
; NUMBER OF SEQ ID NOS: 630
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HUMAN
US-60-245-228-374

Alignment Scores:
Pred. No.: 2.63e-146      Length: 373
Score: 1897.50           Matches: 373
Percent Similarity: 95.15%      Conservative: 0
Best Local Similarity: 95.15%    Mismatches: 0
Query Match: 74.12%           Indels: 19
DB: 27                      Gaps: 1

US-09-935-124A-1 (1-1422) x US-60-245-228-374 (1-373)

Oy 102 ATGACACCTTTGGGGGACCTGCGGAGCCGCGGCGCTGCGCGCGCGCGGAGAA 161
Db 1 MetAspLeuPheGlyAspLeuProGluProGluArgSerProArgProAlaIleLys 20
Oy 162 GAAGTCAAGAAAGACCCCTGCTTTGATGACCTCCCTCCGGCCAGAGTACTGACTCA 221
Db 21 GluAlaGlnLysGlyProLeuLeuPheAspLeuProProAlaSerSerThr----- 38
Oy 222 GGATCAGGGGACCTTTGCTTTTGTATGATCTCCACCCGCTAGCAGTGCAGATTCAAGT 281
Db 39 -----AspSerGly 41
Oy 282 TCTCTTGGCCACATCATATCCCAAGTGTAAAGACTGAAGGAGAAAGACCAAGAGAAA 341
Db 42 SerLeuAlaThrSerIleSerGlnMetValLysThrGlnGlnGlyValAlaLysArgLys 61
Oy 342 ACCTCCGAGAGAGAGAAAGATGGACACTGTGTAAGGAGAAAGATTGTAAAGCC 401
Db 62 ThrSerGlnGlnGlnLysAsnGlySerGlnGlnLysValGlnLysValCysLysAla 81
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[illegible]

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Db 222 GYAAGVALLLEUGLVALLEUGLVALSERARGSERILEGLYASPGILYGLINTYLYSAAG 241
QY 1002 TCGCGGTGACCTCTGTGCGCCGACATCAGACGCTGCAGCTGACCCCGCATGACAGGTTTC 1061
Db 242 CysGlyValThrSerValProAspIleArgIleArgCysGlnLeuThrProAsnAspArgPhe 261
QY 1062 ATTTGTGGCTGTGATGGGCTCTTCAAGTCTTTTACCCAGAAAGACCCGTGAACCTTC 1121
Db 262 IleLeuLeuAlaCysAspGlyLeuPheValPheThrProGluGluValAlaValAsnPhe 281
QY 1122 ATCTTGCTGTCTGTGAGATGAAAGATCCAGACCCGGGAAAGGAAAGTCCCGAGCCGAC 1181
Db 282 IleLeuSerCysLeuGluAspGluValIleGlnThrArgGluGlyLysSerAlaIleAsp 301
QY 1182 GCCCGCTACGAAGACGCTGCAACAGGCTGGCCCAACAGGCGGTGACGGGGCTCGGCC 1241
Db 302 AlaArgIleGluAlaAlaCysAsnArgLeuAlaAsnIleValAlaGlnArgGlySerAla 321
QY 1242 GACAACTGACTGTGATGGTGTGGATAGGCGAC 1277
Db 322 AspaenValThrValMetValValArgIleGlyHis 333

RESULT 19
US-60-229-518-348
; Sequence 348, Application US/60229518
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1000778
; CURRENT APPLICATION NUMBER: US/60/229,518
; CURRENT FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 333
; TYPE: PRT
; ORGANISM: HUMAN
US-60-229-518-348

Alignment Scores:
Pred. No.: 1,296-128 Length: 333
Score: 1681.50 Matches: 333
Percent Similarity: 84.95% Conservatve: 0
Best Local Similarity: 84.95% Mismatches: 0
Query Match: 65.68% Indels: 59
Db: 27 Gaps: 1

US-09-935-124a-1 (1-1422) x US-60-229-518-348 (1-333)
QY 102 ATGACCTCTTGGGGGAGCTGCGGAGCCGCGCGCGCGCGCGCTGCCGGGAAA 161
Db 1 MetAspLeuPheGlyAspLeuProGluProGluArgSerProArgProAlaIleGlyLys 20
QY 162 GAAGCTCAGAAAGACCCCTGCTTTGTGATGACCTCCCTCCGGCAGCAGTACTGCTCA 221
Db 21 GluAlaGlnIleGlyProLeuLeuPheAspLeuProProAlaSerSerThrAspSer 40
QY 222 GATCAGGGGGAACCTTGTCTTTTGTGATGATCTCCACCCGCTAGCAGTGGCATTCAAGT 281
Db 40 ----- 40
QY 282 TCTCTTGCACATCAATATCCAGATGTAAAGACTGAAGGAAAGAGCAAGAAAA 341
Db 40 ----- 40
QY 342 ACCTCCGAGAGAGAGAGAAATGACAGTGAAGACTTGTGAAAAAGAAAGTTGTAAGCC 401
Db 41 -----Ala 41
QY 402 TCTTGGTGATCTTTGTCTGTGAAGGCTATGTGCTGACGAGAGGCTGAGAGGAGAG 461

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Db 42 SerSerValIlePheGlyLeuLysGlyTyrValAlaGluArgLysGlyGluArgGluGlu 61
QY 462 ATGACAGATGCCACGATCTCTGAACGACATCACCAGAGATGATAGGCCCCCATGCTCC 521
Db 62 MetGlnAspAlaIleValIleLeuAsnAspIleIleGlnGluCysArgProProSerSer 81
QY 522 CTCAATTACTCGGGTTTCATATATTTGCTGTTTGTATGATGACATGAGAGAAATTCAGCTCA 581
Db 82 LeuIleThrArgValSerTyrPheAlaValPheAspGlyHisGlyIleArgIleAsp 101
QY 582 AAATTTGCTGCACAAATTTTGATCAAACTTAATCAGAAAAATTTCTTAAGAGATGTA 641
Db 102 LysPheAlaAlaGlnAsnLeuIleGlnAsnLeuIleArgLysPheProLysGlyAspVal 121
QY 642 ATCAGTGTAGAGAAAACCGTAGAGATGCCCTTTTGGACACTTTCAGACATCTGATGAA 701
Db 122 IleSerValGluLysThrValLysArgCysLeuLeuAspThrPheLysHisThrAspGlu 141
QY 702 GAGTTCCTTAAACAACTTCCAGCCAGAACCTGCTGGAAAGATGGGTCCACTGCCAG 761
Db 142 GluPheLeuLysGlnAlaSerSerGlnLysProAlaIleTyrLysAspGlySerThrAlaThr 161
QY 762 TGTGTTCTGGCTGTGACAACTTTTATATTCGCAACTTCGAGATATGCGGGCAATC 821
Db 162 CysValLeuAlaValAspAsnIleLeuTyrIleAlaAsnLeuGlyAspSerArgAlaIle 181
QY 822 TTGTGCTGTTAATAGAGAGAGTCAAAAACATGACGCTTAAGCTCAGCAAAAGAGAT 881
Db 182 LeuCysArgIleAsnGluGluSerGlnLysHisAlaAlaLeuSerLeuSerLysGluHis 201
QY 882 AATCCAACTCAATATGAAGCGGATGAGATACAGAAAGCTGAGAGAACTCAGGAGAT 941
Db 202 AsnProThrGlnTyrGluGluArgMetArgIleGlnLysAlaGlyLysValAlaArgAsp 221
QY 942 GGGCGTGTGTTGGGCGCTGTAGAGGTGCAGCTCATTGGGAGCGGCGCATGACAGGC 1001
Db 222 GYAAGVALLLEUGLVALLEUGLVALSERARGSERILEGLYASPGILYGLINTYLYSAAG 241
QY 1002 TCGCGGTGACCTCTGTGCGCCGACATCAGACGCTGCAGCTGACCCCGCATGACAGGTTTC 1061
Db 242 CysGlyValThrSerValProAspIleArgIleArgCysGlnLeuThrProAsnAspArgPhe 261
QY 1062 ATTTGTGGCTGTGATGGGCTCTTCAAGTCTTTTACCCAGAAAGACCCGTGAACCTTC 1121
Db 262 IleLeuLeuAlaCysAspGlyLeuPheValPheThrProGluGluValAlaValAsnPhe 281
QY 1122 ATCTTGCTGTCTGTGAGATGAAAGATCCAGACCCGGGAAAGGAAAGTCCCGAGCCGAC 1181
Db 282 IleLeuSerCysLeuGluAspGluValIleGlnThrArgGluGlyLysSerAlaIleAsp 301
QY 1182 GCCCGCTACGAAGACGCTGCAACAGGCTGGCCCAACAGGCGGTGACGGGGCTCGGCC 1241
Db 302 AlaArgIleGluAlaAlaCysAsnArgLeuAlaAsnIleValAlaGlnArgGlySerAla 321
QY 1242 GACAACTGACTGTGATGGTGTGGATAGGCGAC 1277
Db 322 AspaenValThrValMetValValArgIleGlyHis 333

RESULT 20
PCT-US01-08631-40296
; Sequence 40296, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736

```

SOFTWARE: Custom
SEQ ID NO: 40296
LENGTH: 378
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: DOMAIN
LOCATION: (129) ..(139)
OTHER INFORMATION: Protein phosphatase 2C proteins domain identified by EMATRIX,
OTHER INFORMATION: accession number BL01032C, p-value=3.195e-12, raw score of 6.14
PCT-US01-08631-40296

Alignment Scores:

Pred. No.	Score:	Length:
3,15e-110	1457.50	378
Best Similarity:	81.23%	Matches: 303
Best Local Similarity:	77.89%	Conservative: 13
Query Match:	56.93%	Mismatches: 46
		Gaps: 27
		Indels: 6

US-09-935-124A-1 (1-1422) x PCT-US01-08631-40296 (1-378)

DY 159 AAGAGAAGCTGAGAAAGAACCCCTGGCTTTATACCTCCCGGACAGACTGAC 218
Db 1 LysglunlaglnylsglyProleuleuPheaprepneuPropoalaserthrpsp 20
DY 219 TCAGAGATCAAGGGGACCTTGTCTTTTGATGATCCCAACCCGTCAGCATGCA 278
Db 21 Serla-----ValAlalauglyThrThr 29
DY 279 GCTTCTCTGCACATCAATGCCAGATGTAAGACCTGAAGGAAAGCAAGAGA 338
Db 30 ProserProvalhrleutrpheleuglnhrArgrglserylletrrphagn 49
DY 339 AAAACCTCCAGAGAGAAAGAAATGGCACGTGAAGCTTGCGAAAAGAAAGTTGTA 398
Db 50 Serleuabpryrglnserlysvallglyalnuprotprcyshisglumaglnly 69
DY 399 -----GCCTCTTGGGTGATCTTTGGTCTG 422
Db 70 AlaapArgpheleuglylsarglyArvalProalasersevalillepeghlyeu 89
DY 423 AAGGCTATGTGGCTGACCGAAGGGTGAAGAGAGAGATGACGAGTCCGATC 482
Db 90 LysgllyrValalaglualrglysglyuaAgglungluMetglnabpahlstalle 109
DY 483 CTGAACGACATCACCGAGAGGTAGGCCCCCATGTCCTCCATTACTCGGTTTTATAT 542
Db 110 LeuendaprllethrnglucysArgproposerSerleuilethrArgrValserTy 129
DY 543 TTTGGCTTTTATGACATGAGAAATTCAGAGCTCAAAATTTGTCGACAGAAATTTG 602
Db 130 PhealavalPheaprglyshisgllylleArglaserlysphealialaiglnanleu 149
DY 603 CATCAAACCTTAACAAGAAATTTCTTAAGAGAGATGATACATGATGAGAAACCGG 662
Db 150 HisglinanleuValaiglysheproulysglyArvalilleserValglulystrVal 169
DY 663 AAGAGATCCCTTTGACACTTCAAGCATCTGAATGAAGATTCCTTAACAAGCTCC 722
Db 170 LysargylseuLeuabprlnrPheulshisthrAprglucunpneleuylsglnalas 189
DY 723 AGCGAAGAGCTGCTGGAAGATGGGTCACTGCCAGTGCTGTTGGCTGATGACAC 782
Db 190 SerGlnlyspProalatrplyAspglysetrmAlamrcCyvalLeuAlavalaspen 209
DY 783 ATTCTTATATATGCGAACCTCGAGATAGTCGGGCAATCTTGTCGTTATATAGAGG 842
Db 210 HleuuryrlllealasnleuglyaspserArgalalleuencysArglyrAmglunglu 229

QY 843 AGTCAAAAACATGACGACCTTAAGCTTCAGACAAAGACATTAATCCAACTCAAGTATGAAAG 902

Db 230 SerGlnLysHisAlaIalaIeuSerLysSerLysGlnHisAAspProthGlnTyrGlnGlu 249

QY 903 CGGATAGAGATACAGAAAGGCTTGAGAGAAACCTCAGGAGATGGCGTGTGTTTGGCGGTGCTA 962

Db 250 ArgMetIrrGlnGlnLysAlaGlyGlyAAsnValAraAAspGlyAraValLeuGlnValLeu 269

QY 963 GAGGTGACAGCTTCATTTGGGAGCGGACAGTAAAGCGCTGGCGTGC---ACCTCTGTG 1019

Db 270 GlnValSerIrrSerLysGlnValAAspGlyGlnTyrLysArgCysGlnLysLeuGlnA 289

QY 1020 CCGACATCAGACGCGTGCAGTACGCCCAATGACAGTTCATTTGTTG---GCCGTG 1076

Db 290 ProthSerIrrArgIrrCysGlnLysLeuThrProAspIrrSerPheIrrLeuValIrrProCys 309

QY 1077 GATGGGCTCTTCAAGTCTTTATCCCGAAGAGAGCGTGAACTTCATCTTGGCTGTGCTC 1136

Db 310 AspGlyLeuMetLysValAlaPheThrProGlnGlnAlaValAsnPheIrrLeuSerCysLeu 329

QY 1137 GAGGATGAAAGATCCAGACCCGGAGAGGAAAGTCCGACGCGACGCCCGCTACAGAAAGCA 1196

Db 330 GlnAspGlnLysLysIrrGlnThrArgGlnLysLysSerAlaHisAAspValIrrLeuArgSer 349

QY 1197 GCC---TGCAACAGCGCTGSCCAACAGCGCGGTGCAGCGGGGCTCG---GCCACAAAGTC 1250

Db 350 SerProAlaThrIrrArgLeuAlaAsnLysAlaValAlaIrrValAraArgProAspMetVal 369

QY 1251 ACTGTGATGGTGGTGGCGGATAGGAGC 1277

Db 370 ThrValMetValAlaArgIrrGlnHis 378

RESULT 21

US-10-147-874-3

/ Sequence 3, Application US/10147874

/ GENERAL INFORMATION:

/ APPLICANT: TARDIEUX, ISABELLE

/ APPLICANT: DELOME, VIOLENE

/ TITLE OF INVENTION: SEICINE-THREONINE PHOSPHATASE PROTEIN OF A PARASITIC ORGANISM OF T

/ TITLE OF INVENTION: AINCOMPLEXA PHYLM, APPLICATIONS IN THERAPEUTICS

/ FILE REFERENCE: 22316USO

/ CURRENT APPLICATION NUMBER: US/10/147, 874

/ CURRENT FILING DATE: 2002-05-20

/ PRIOR APPLICATION NUMBER: US 60/291,609

/ PRIOR FILING DATE: 2001-05-18

/ SOFTWARE: PatentIn version 3.1

/ NUMBER OF SEQ ID NOS: 19

/ SEQ ID NO 3

/ LENGTH: 248

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-147-874-3

Alignment Scores:

Pred. No.: 1,69e-95 Length: 248

Score: 1277.00 Matches: 248

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 49.88% Indels: 0

Db: 25 Gaps: 0

US-09-935-124A-1 (1-1422) x US-10-147-874-3 (1-248)

QY 522 CTCATTAAGTCGGGGTTTCAATATTTTGTGTTTGGATGACATGAGAGATTCGAGCTCA 581

Db 1 LeuIrrThrArgValSerIrrPheAlaValPheAspGlyHisGlyGlyIrrLeuGlnAAser 20

QY 582 AAATTTGGTGGAGATTTTGGATCAAACTTAATCAAGAAAATTTCTTAAGAGATGTA 641

Db 21 LysPheIrrAlaIrrGlnIrrAsnLysHisGlnIrrLeuIrrLeuIrrGlySerProLysGlnValAspVal 40

QY 642 ATCAAGTGAAGAAACCCTGAAGAGATGCTTTTGGACACTTTCAAGCATACTGATGA 701

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Db 41 IIESeValGIuLyThrValIySArGyCyLeuLeuAspThrPhySerHisThrIAspGlu 60
Qy 702 GAGTTCCTTAACAAAGCTTCAGACGCAAGAGCTGCTGGAAAGATGGGTCCATGCGCAG 761
Db 61 GIuPhLeuLeuSbGlnIAspSerGlnIySProAlaITrIyAspSbIySerThrIAspThr 80
Qy 762 TGTGTTCTGGCTGTAGACAACATTTCTTATATTGCAACCTCGAGATAGTGGGCAATC 821
Db 81 CyValIleuAlaValAspSerHisIleuTyrlIeAlaAsnIleuIyAspSerArgAlaIle 100
Qy 822 TTGTGCTTATTAATAGAGAGACTCAAAAACATGACGCTTAAGCTTCAGCAAGAGCAT 881
Db 101 LeuCyArGlyTrAsnGlnIuGlnSerGlnIySbHsAlaAlaIeUserIeUserIySbIuHs 120
Qy 882 AATCCAACTCAGATGAAGACGAGATGAGATACAGAAAGGCTGAGAAACGTCAGAGAT 941
Db 121 AsnProThGIInTyrlGlnIuGlnMetArgIleGlnIyAspIAspIyAsnValIAsp 140
Qy 942 GGGCGGTGTTGGGCGTGTAGAGGTGTCACTGCTCATTTGGGAGCGGAGTACAAAGCC 1001
Db 141 GIyArGValIleuGlyValIleuGlnIySArGSerIleGIyAspGIyInTyrlIySArG 160
Qy 1002 TGGCGGTGTCACCTCTGTGCGCCGACATCAGACGCTGCGCAGCTGACCCCAATGACAGTTT 1061
Db 161 CySGIyValThSerValIProAspIleArGArGyCySGIleuThrProAsnSbArGpHe 180
Qy 1062 ATTTGTTGGCTGTGATGGGCTCTTCAAGGTCTTTACCCAGAAAGACGCGGAACTTC 1121
Db 181 IIEleuLeuAlaCyAspSbIyLeuPhyValIAspThrProIuGlnIAlaValAspHe 200
Qy 1122 ATCTGTCTGTCTGTGAGATGAAAGATTCAGACCGGAGAGGAAGTCCGAGCGAG 1181
Db 201 IIEleUserCyLeuGlnIuAspGIuIySleGIInThrArgGIuGIyIySserAlaIAsp 220
Qy 1182 GCGCGGTAGAGAGACCTTCGCAACAGCGTGGCCAAACAAGCGGTGACGCGGCTCGGCC 1241
Db 221 AIAArGlyrGIuAlaIaCyAsnArGlyLeuAlaAsnIySAlaValaGIInrGIySerAla 240
Qy 1242 GACAACGTCACTGTGATGGTGTG 1265
Db 241 AspAsnValThrValMetValVal 248

RESULT 22
PCT-US01-08631-40295
; Sequence 40295, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 40295
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (184)..(194)
; OTHER INFORMATION: Protein phosphatase 2C proteins domain identified by eMATRIX,
; OTHER INFORMATION: accession number B101032C, p-value=3.195e-12, raw score of 6.14
; LOCATION: (144)..(211)
; OTHER INFORMATION: Protein phosphatase 2C domain identified by Pfam, accession
; OTHER INFORMATION: name PP2C, E-value=9.2e-09, Pfam score of 34.3
PCT-US01-08631-40295

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Alignment Scores:
Pred. No.: 3,77e-77 Length: 221
Score: 1053.00 Matches: 206
Percent Similarity: 96.26% Conservative: 0
Best Local Similarity: 96.26% Mismatches: 0
Query Match: 41.13% Indels: 8
DB: 1 Gaps: 1

US-09-935-124A-1 (1-1422) x PCT-US01-08631-40295 (1-221)
Qy 36 TGGAGCCGCGCGCTGCTCGCGGGGAGTGTCTGCTGCTGCGGCTCCAGCCAGCC 95
Db 8 TrpSerProAlaAlaIAspGIyLeuSerValCySArGyCySArGleuHisProAla 27
Qy 96 TCCGCCATGAGCTCTTTCGGGAGCTGCGGAGCCGAGCGCTGCGCGCGCGCTGCGC 155
Db 28 SerAlaMetAspLeuPhcGIyAspLeuProGIuProGIuArGSerProArGProAlaIa 47
Qy 156 GGGAAAGAACTCAGAAAGAGACCCCTGCTTTGATGACTTCCTCCGCGCAGCACTACT 215
Db 48 GIySGIuAlaGlnIySGIyProleuLeuPhcAspLeuProAlaIAspSerThr 67
Qy 216 GACTCA-----GGATCAGGGGAGCTTTGCTTTTGATGAT 251
Db 68 AspSerGIySerSerIeuglnAlaIeUProGIySerGIyGIyProleuLeuPhcAsp 87
Qy 252 CTCCACCGCTAGAGAGTGGCGATTCAGGTTCTCTTGCCACATCAATATCCAGATGTA 311
Db 88 LeuProProIAspSerSerGIyAspSerGIySerIeUAlaIAspThrSerIleSerIleMetVal 107
Qy 312 AAGACTGAAGGAAAGAGCAAAAGAAAACCTCCGAGAAAGAGAAAGATGGCAGTGA 371
Db 108 IySThGIuGIyGIyAlaIyAspArGIySThSerGIuGIuGIyAbnGIySerGIu 127
Qy 372 GAGCTTGTGGAAGAAAGTTGTAAAGCTCTTGGGAGATTTGTGTGAAGGCTAT 431
Db 128 GIuLeuValaGIuLySbValaCySbIySbIAspSerValIIEpHeGIyLeuIySbGIy 147
Qy 432 GTGCGTGAAGCGGAGGTGAGAGAGAGAGATGACAGATGCCACGTATCTTGAAGCAG 491
Db 148 ValAlaGIuArGIyGIyGIuArGIuGIuMetGlnAspAlaIAspValaIIEuAsnSb 167
Qy 492 ATCACCAGAGAGTGTAGGCCCCCATGTCCTCATTTACTCGGGTTTCATATTTTGTGTT 551
Db 168 IIEThGIuGIuCyArGProProSerSerIeUleIIEThArGValSerTyzrPhcAlaVal 187
Qy 552 TTTGATGACATGAGAGAAATTCGAGCTCAAAATTTGCTGCAACAATTTGATCAAAAAC 611
Db 188 PhcAspGIyHisGIyGIyIIEArGAlaSerIySPhcAlaAlaGIInAsnIuHsGIInAsn 207
Qy 612 TTAATCAGAAATTTCTTAAGAGATGTAATCAGTGTAGAG 653
Db 208 LeuIIEArGIySbPhcProIySbIyAspValIIESerValGIu 221

RESULT 23
US-09-791-537-134656
; Sequence 134656, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134656
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-791-537-134656

```

Alignment Scores: 4,81e-61 Length: 167
 Pred. No.: 856.00 Matches: 165
 Score: 99.40% Conservative: 1
 Percent Similarity: 98.80% Mismatches: 1
 Best Local Similarity: 98.80% Indels: 0
 Query Match: 33.44% Gaps: 0
 DB: 21

US-09-935-124a-1 (1-1422) x US-09-791-537-134656 (1-167)

QY 570 ATTGAGCCTCAAAATTGCTGACAGAAATTGCACTAACTTAATCAGAAATTTCT 629
 DB 1 TLeTgAlAserLyLeuAlaAGInAsenLeuH1sgInAsenLeuIleArGlySPhePro 20

QY 630 AAAGAGATGTATCATAGTGTAGAGAAAACCGTAGAAGATGCTTTTGAACACTTTCAG 689
 DB 21 LyeGlyAspIleIleSeVaIGluYThValYSArGySbleuLeuAspThrPheLyS 40

QY 690 CATACTGATGAAGATTCTTAAACAAGCTTCCAGCAGAAAGCCTGCTGAAAAGATGGG 749
 DB 41 H1eThrAspGluGluPheLeuLyGlnAlaSerSerGlnLySProAlaTrpLyAspGly 60

QY 750 TCCATGCGCAGGTGTGTTGCTGCTGTAGACAACATCTTTATTTGCAACCTCGAGAT 809
 DB 61 SerThAlaThrCySeValLeuAlaValAspAsnIleuYrIleAlaAsenLeuGlyAsp 80

QY 810 AGTCGGGCAATCTGTGCTGTATTAATGAGAGAGATCAAAAACATGACGCTTAAGCTC 869
 DB 81 SerThAlaIleLeuCyAspGlyAspGluGluSerGlnLySAsnAlaAlaLeuSerLeu 100

QY 870 AGCAAGAGCATTAATCCACTCACTAGTAAGAACCGATAGATACAGAAAGCGTAGAGA 929
 DB 101 SerLyGluH1AspIleArGlyValLeuGlyValLeuGlyValSerAspSerIleGlyAspGly 120

QY 930 AACGTACGAGATGCGCTGTTTGGCGCTGAGGTGTCACGCTCCATTGGGACGGG 989
 DB 121 AsnValArAspGlyArGlyValLeuGlyValLeuGlyValSerAspSerIleGlyAspGly 140

QY 990 CAGTACAGCGCTGCGGTGTCACTCTGTGCTCCGACATAGACGCTGCGACGTGACCCCC 1049
 DB 141 GlnTrpLyArGyCyGlyValThSerValProAspIleArGyArGyGlnLeuThrPro 160

QY 1050 AATGACAGGTTCATTGTTGTTG 1070
 DB 161 AsnAspArGpHeIleLeuLeu 167

RESULT 24
 US-09-834-366-15305 Application US/09834366
 GENERAL INFORMATION:
 APPLICANT: Bejantin, Stephane
 APPLICANT: Tanaka, Hiroaki
 APPLICANT: Dumas Milne Edwards, Jean Baptiste
 APPLICANT: Jobert, Severin
 APPLICANT: Giordano, Jean-Yves
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: 81 US2 P83
 CURRENT APPLICATION NUMBER: US/09/834,366
 CURRENT FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: US 60/197,873
 PRIOR FILING DATE: 2000-04-18
 NUMBER OF SEQ ID NOS: 52153
 SOFTWARE: Patent.pm
 SEQ ID NO 15305
 LENGTH: 123
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-834-366-15305

Alignment Scores: 2.56e-42 Length: 123
 Pred. No.: 627.00 Matches: 123
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 24.49% Gaps: 0
 DB: 27

US-09-935-124a-1 (1-1422) x US-09-791-537-134656 (1-167)

QY 570 ATTGAGCCTCAAAATTGCTGACAGAAATTGCACTAACTTAATCAGAAATTTCT 629
 DB 1 TLeTgAlAserLyLeuAlaAGInAsenLeuH1sgInAsenLeuIleArGlySPhePro 20

QY 630 AAAGAGATGTATCATAGTGTAGAGAAAACCGTAGAAGATGCTTTTGAACACTTTCAG 689
 DB 21 LyeGlyAspIleIleSeVaIGluYThValYSArGySbleuLeuAspThrPheLyS 40

QY 690 CATACTGATGAAGATTCTTAAACAAGCTTCCAGCAGAAAGCCTGCTGAAAAGATGGG 749
 DB 41 H1eThrAspGluGluPheLeuLyGlnAlaSerSerGlnLySProAlaTrpLyAspGly 60

QY 750 TCCATGCGCAGGTGTGTTGCTGCTGTAGACAACATCTTTATTTGCAACCTCGAGAT 809
 DB 61 SerThAlaThrCySeValLeuAlaValAspAsnIleuYrIleAlaAsenLeuGlyAsp 80

QY 810 AGTCGGGCAATCTGTGCTGTATTAATGAGAGAGATCAAAAACATGACGCTTAAGCTC 869
 DB 81 SerThAlaIleLeuCyAspGlyAspGluGluSerGlnLySAsnAlaAlaLeuSerLeu 100

QY 870 AGCAAGAGCATTAATCCACTCACTAGTAAGAACCGATAGATACAGAAAGCGTAGAGA 929
 DB 101 SerLyGluH1AspIleArGlyValLeuGlyValLeuGlyValSerAspSerIleGlyAspGly 120

QY 930 AACGTACGAGATGCGCTGTTTGGCGCTGAGGTGTCACGCTCCATTGGGACGGG 989
 DB 121 AsnValArAspGlyArGlyValLeuGlyValLeuGlyValSerAspSerIleGlyAspGly 140

QY 990 CAGTACAGCGCTGCGGTGTCACTCTGTGCTCCGACATAGACGCTGCGACGTGACCCCC 1049
 DB 141 GlnTrpLyArGyCyGlyValThSerValProAspIleArGyArGyGlnLeuThrPro 160

QY 1050 AATGACAGGTTCATTGTTGTTG 1070
 DB 161 AsnAspArGpHeIleLeuLeu 167

RESULT 25
 US-60-197-873-15305 Application US/60197873
 GENERAL INFORMATION:
 APPLICANT: Bejantin, Stephane
 APPLICANT: Tanaka, Hiroaki
 APPLICANT: Dumas Milne Edwards, Jean Baptiste
 APPLICANT: Jobert, Severin
 APPLICANT: Giordano, Jean-Yves
 TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 FILE REFERENCE: 81 US1 P80
 CURRENT APPLICATION NUMBER: US/60/197,873
 CURRENT FILING DATE: 2000-04-18
 NUMBER OF SEQ ID NOS: 52153
 SOFTWARE: Patent.pm
 SEQ ID NO 15305
 LENGTH: 123
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-60-197-873-15305

Alignment Scores: 2.56e-42 Length: 123
 Pred. No.: 627.00 Matches: 123
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 24.49% Gaps: 0
 DB: 27

US-09-935-124a-1 (1-1422) x US-60-197-873-15305 (1-123)

QY 102 ATGACCTCTTGGGGAGACCTGCGGAGCCGAGACGCTGCGCGCGGCTGCGGGAAA 161
 DB 1 MetAspLeuPheGlyAspLeuProGluProGluArGSerProArGProAlaIleGlyLe 20

QY 162 GAAGCTCAGAAAGAACCCCTGCTTTGATGACCTCCCTCGGACGAGATGACTCA 221
 DB 21 GlnAlaGlnLyGlyProLeuLeuPheAspLeuProAlaSerSerThAspSer 40

QY 222 GAATCAGGGGACCTTTGCTTTTGAATCTCCACCGCTAGAGATGGGATTCAGGT 281
 DB 41 GlySerGlyProLeuLeuPheAspLeuProAlaSerSerThAspSer 60

QY 282 TCTCTGCCACATCAATATCCAGATGCTAAGACTGAAGGAAAGGACAAAGAAA 341
 DB 61 SerLeuAlaThrSerIleSerGlnMetValLyThrGluGlyValAlaLySArGlyS 80

QY 342 ACCTCCAGAGAAAGAAATGCGAGATGGAAGCCTTGAGAAAAGATTTGTAAGCC 401
 DB 81 ThrSerGluGluGluValAspGlySerGluGluLeuValGluLyValCySArGlySA 100

QY 402 TCTTCGATGATCTTTGCTGCTGAGAGGCTATGTGCTGAGCGGAGGATGAGAGAG 461
 DB 101 SerSerValIlePheGlyLeuLyGlyTYrValAlaGlyArGlyGlyArGlyGlu 120

QY 462 ATGCAAGAT 470
 DB 121 MetGlnAsp 123

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 24.49% Indels: 0
 DB: 22 Gaps: 0

US-09-935-124a-1 (1-1422) x US-09-834-366-15305 (1-123)

QY 102 ATGACCTCTTGGGGAGACCTGCGGAGCCGAGACGCTGCGCGGCTGCGGGAAA 161
 DB 1 MetAspLeuPheGlyAspLeuProGluProGluArGSerProArGProAlaIleGlyLe 20

QY 162 GAAGCTCAGAAAGAACCCCTGCTTTGATGACCTCCCTCGGACGAGATGACTCA 221
 DB 21 GlnAlaGlnLyGlyProLeuLeuPheAspLeuProAlaSerSerThAspSer 40

QY 222 GAATCAGGGGACCTTTGCTTTTGAATCTCCACCGCTAGAGATGGGATTCAGGT 281
 DB 41 GlySerGlyProLeuLeuPheAspLeuProAlaSerSerThAspSer 60

QY 282 TCTCTGCCACATCAATATCCAGATGCTAAGACTGAAGGAAAGGACAAAGAAA 341
 DB 61 SerLeuAlaThrSerIleSerGlnMetValLyThrGluGlyValAlaLySArGlySA 80

QY 342 ACCTCCAGAGAAAGAAATGCGAGATGGAAGCCTTGAGAAAAGATTTGTAAGCC 401
 DB 81 ThrSerGluGluGluValAspGlySerGluGluLeuValGluLyValCySArGlySA 100

QY 402 TCTTCGATGATCTTTGCTGCTGAGAGGCTATGTGCTGAGCGGAGGATGAGAGAG 461
 DB 101 SerSerValIlePheGlyLeuLyGlyTYrValAlaGlyArGlyGlyArGlyGlu 120

QY 462 ATGCAAGAT 470
 DB 121 MetGlnAsp 123

```
Oy 222 GGATCAGGGGGA CTTTGGCTTTTGA TGA TCTCCACCCGCTAGCAGTGGCATTCAGGT 281
Db 41 GlysSerGlyGlyProleuLeuPheAspApleuProAlaSerSerGlyAspSerGly 60
Oy 282 TCTCTTGCCACATCAATATCCCA GATGTAAGACTGAAGGGAAGAGCAAGAGAAA 341
Db 61 SerLeuAlaThrSerIleSerGlnMetValLysThrGluGlyLysGlyAlaLysArgLys 80
Oy 342 ACCTCGAGAGAGAGAAATGGCA GGTGAAGACTTGGAAGAAAGATTGTAAAGCC 401
Db 81 ThrSerGluGluGlnLysAsnGlySerGluGluLeuValGluLysLysValCysLysAla 100
Oy 402 TCTTCGGTATCTTTGGCTGAAG GCTATGTGCTGAGCGAGAGGCTGAGAGGAGAG 461
Db 101 SerSerValIlePheGlyLeuLysGlyTyrValAlaGluArgLysGlyGluArgGluGlu 120
Oy 462 ATGCAGGAT 470
Db 121 MetGlnAsp 123
```

Search completed: February 9, 2003, 18:10:37
Job time : 323.5 secs

OTHER INFORMATION: Serine/threonine phosphatases, family 2C,
OTHER INFORMATION: catalytic domain
US-10-072-012-853

Alignment Scores:
Pred. No.: 2,91e-20 Length: 260
Score: 422.50 Matches: 103
Percent Similarity: 56.18% Conservative: 56
Best Local Similarity: 36.40% Mismatches: 93
Query Match: 16.50% Indels: 31
Gaps: 6

US-09-935-124a-1 (1-1422) x US-10-072-012-853 (1-260)

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OY 417 GGTCTGAGAGGCTATGTGCTGAGCGAGAGGCTGAGAGGAGAGATGACGAGATGCCAC 476
Db 9 G1yleuArgTyrG1yLysSerSerMetGlnG1yValArgLysPrometGluAspAlaHis 28
OY 477 GTGATCTGAGACGATCAGGAGAGTGTAGAGGCCCATGTGCTCATTAATCTCGAGTT 536
Db 29 ValIleThrProAspLeuSerG1yGlu-----AspSerG1y 40
OY 537 TCATATTTGCTGCTTTTGTGATGACATGAGCAATTCGAGCCTCAAAATTTGCTGCACAG 596
Db 41 G1yPheHeG1yAlpPheAspD1yHisG1ySerGluAlaAlaLysPheLeuSerLys 60
OY 597 AATTGATCAAAACTTAATCAGAAATTTCTTAAAGAGATGTATCAGTATGAGAA 656
Db 61 AsnLeuProGluIleLeuAlaGluGluLeuIleLysAspLys-----AspGluAspGlu 78
OY 657 ACCGTGAGAGATGCTTTTGGACATTTTCAGCATATCTGATGAAGAGTCTTTAAACAA 716
Db 79 AspValGluAspAlaLeuArgLysAlaPheLeuArgThrAspGluIleLeuGluGlu 98
OY 717 GCTTCCAGCCAGAGCCTGCTCGAAGATGGGTTCACCTGCCACGTGTGTTCTGGCTGA 776
Db 99 LeuGluSerLeuGluAspGln---ArgSerG1yThrThAlaValAlaLeuIleArg 117
OY 777 GACAAATCTTTATATTCGCAACTCGAGATGATGTCGCGCAATCTTGTCGTATATAT 836
Db 118 G1yAsnLysLeuTyrValAlaAsnValG1yAspSerArgAlaValIleuCyAsArgAngly 137
OY 837 GAGGAGAGTCMAAAACATGCAAGCCTTAGCCTTCAGCAAGACATATTCACAATCACTAT 896
Db 138 Lys-----AlaValGluLeuThrGluAspHisLeuProSerArgAnglu 151
OY 897 GAAAGCGGATGAGATACAGAAAGCTGAGAGAAAGCTCAGGAGTGGGCTTTGGGC 956
Db 152 AspGluArgGluArgLysLeuArgLysAlaG1yPheValSerAsnG1yArgValAsnGly 171
OY 957 GTGCTAGAGGTTCACGCTCCATTTGGGACGCGCAGTACAGAGCGCTCGCTCACTCT 1016
Db 172 ValLeuAlaLeuSerArgAlaLeuG1yAsp---PhePheLeuLysProTyrValIleAla 190
OY 1017 GTGCCGACATCAGACGCTGCCAGCTGACCCCCAATGACAGTTTCATTTGTGGCTGT 1076
Db 191 GluProAspValThrValValGluLeuThrG1yAspAspPheLeuIleLeuAlaSer 210
OY 1077 GATGGGCTCTTCAAGGCTTTTACCCGAGAGAGAGCCGTGAATCTTCTGTCTCTC 1136
Db 211 AspG1yLeuTyrAspValIleuSerAsnGlnG1yValAlaAspIleVal----- 226
OY 1137 GAGGATGAAAAGATCCAGACCCGAGAGGAGTCCGACCCGACCCGCTACGAGACA 1196
Db 227 -----ArgLysHisLeuSerLysG1yG1yProGlnGlu 237
OY 1197 GCCTGCAAGAGCTGCGCAACAAGCGGTGACGCGGCTCGGCGCAGCAACTCTATGTG 1256
Db 238 AlaAlaLysLysLeuIleAspLeuAlaIleAlaArgG1ySerLysAspAsnIleThrVal 257
OY 1257 ATGTGTGTG 1265
Db 258 ValValVal 260

```

RESULT 3

US-09-513-999C-7505

Sequence 7505, Application US/09513999C

GENERAL INFORMATION:

APPLICANT: Dumas Mline Edwards, J.B.

APPLICANT: Duclet, A. J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59, US2, REG

CURRENT APPLICATION NUMBER: US/09/513, 999C

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122, 487

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent, pm

SEQ ID NO 7505

LENGTH: 86

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: UNSURE

LOCATION: 55

OTHER INFORMATION: Xaa=Phe or Leu

NAME/KEY: UNSURE

LOCATION: 56

OTHER INFORMATION: Xaa=Ala or Pro

NAME/KEY: UNSURE

LOCATION: 65

OTHER INFORMATION: Xaa=Glu or Lys

US-09-513-999C-7505

US-09-513-999C-7505

Alignment Scores:
Pred. No.: 1,59e-19 Length: 86
Score: 411.00 Matches: 83
Percent Similarity: 95.40% Conservative: 0
Best Local Similarity: 95.40% Mismatches: 3
Query Match: 16.05% Indels: 1
Gaps: 0

US-09-935-124a-1 (1-1422) x US-09-513-999C-7505 (1-86)

```

OY 462 ATGCGAGATGCCACGCTCATCTGAAACGACATCACGAGAGTGTAGGCCCATGCTCC 521
Db 1 MetGlnAspAlaHisValIleLeuAsnAspIleThrGluGluCyAsArgProProSerSer 20
OY 522 CTCATTACTCGGGTTCATATTTGCTGTTTGTATGACATGAGAGAAATTCAGAGCTCA 581
Db 21 LeuIleThrArgValSerTyrPheAlaValAlpHeAspD1yHisG1yG1yIleArgAlaSer 40
OY 582 AAATTTGCTGCACAGAAATTTGCATCAAACTTAATCAGAAATTTCTTAAGAGATGTA 641
Db 41 LysPheAlaIleGlnLeuLeuHisGlnLeuLeuIleArgLys*****LysG1yAspVal 60
OY 642 ATCAGTGTAGAGAAACGCTGAAGAGATGCTTTTGGACACTTTCAGAGATCTGATGAA 701
Db 61 ILeSerValGlu***ThrValLysArgCyLeuLeuAspThrPheLysHisThrAspGlu 80
OY 702 GAGTTCCTTAACAAGCTT 720
Db 81 Glu-SerLeuAsnLysLeu 86

```

RESULT 4

US-10-072-012-854

Sequence 854, Application US/10072012

GENERAL INFORMATION:

APPLICANT: Tcherven, Velizar

APPLICANT: Spytek, Kimberly

APPLICANT: Zernusen, Bryan

APPLICANT: Patrujan, Meera

APPLICANT: Shimkets, Richard

```

/ APPLICANT: Li, Li
/ APPLICANT: Gangolli, Esba
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Anderson, David W.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Taupier Jr, Raymond J.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Colman, Steven D.
/ APPLICANT: Wolenc, Adam R.
/ APPLICANT: Pena, Carol E. A
/ APPLICANT: Futak, Katarzyna
/ APPLICANT: Grosse, William M.
/ APPLICANT: Alsobrook II, John P.
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ TITLE OF INVENTION: proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-258
/ CURRENT APPLICATION NUMBER: US/10/072,012
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: 60/265,102
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 854
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Protein
US-10-072-012-854

Alignment Scores:
Pred. No.: 5,3e-19 Length: 252
Score: 403.50 Matches: 104
Percent Similarity: 56.27% Conservative: 53
Best Local Similarity: 37.28% Mismatches: 85
Query Match: 15.76% Indels: 37
DB: 6 Gaps: 10

US-09-935-124A-1 (1-1422) x US-10-072-012-854 (1-252)
QY 432 CTGGCTGACCGAAGGTGAGAGGAGGAGATGCGAGATGCCATCTCATCTGAAGAC 491
DB 5 ValSerArgMetGlnGlyPheArgTyrPheMetGluAspAlaIleIleAlaGlySerAsn 24
QY 492 ATCACCAGAGAGTGTAGGCCCCCATCGCTCATTAATCGGGTTTCATATTTGGTGT 551
DB 25 LeuAsnSerSerGlyGlyLysAspSerLys-----GlyPhePheAlaVal 39
QY 552 TTGATGACATGAGGAATTGAGCCTCAAAATTGTCGACAGATTGATCAAAAC 611
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DB 40 PheArgGlyHisGlyLysSerGlnAlaIleLysTyrAlaGlyLysHisLeuGlnThrLys 59
QY 612 TTA---ATCAGAAA---TTTCTTAAGAGATGTAATCAGTGTGAGAAAACSTGAAG 665
DB 60 LeuAlaLeuArgLysSerPheProGlnLeuAsp-----AspLeuGlnAsnAlaLeuLys 77
QY 666 AGATGCTTTTGGACATTTGACAGCATATGATGAAGATTCCTTAAACAGCTTCCAGC 725
DB 78 GluSerPheLeuGlnSer-----ThrAspGlnGlnLeu-----ArgSerSerAla 92
QY 726 CAGAAGCTGCTGGAAGATGGCTCCAGTCCAGCTGTGTCTTGGCTGTAGAACATTT 785
DB 93 AlaAsnThrAspLeuAspSerLysSerThrAlaValAlaLeuIleArgGlyAsnLys 112
QY 786 CTTTATATGCAACCTGAGAGATAGTGGGCAATCTTGCTGTTATATGAGAGAGT 845
DB 113 LeuTyrValAlaAsnValAlaGlyAspSerArgAlaValLeuGlyValG----- 127
QY 846 CAAAAACATGCAAGCCTTAAGCTCAGCAAAAGACATTAATCCAACTCAATATGAAGCGG 905
DB 128 AsnGlyAsnAlaIleLysGlnLeuThrGlnAspHisLysProSerAsnGlnAspGlnArg 147
QY 906 ATGAGATATCAGAAAGCTGAGGAAACGTC--AGGATGGGCGCTTTTGGCGCTGCTA 962
DB 148 ArgArgGlnGlnGlnGlyAlaGlyLysPheValSerArgAsnGlnArgValAsnGlnValLeu 167
QY 963 GAGTGTCAAGCTCCATTTGGGAGCGGACGATCAAG-----CGTGGCGGTCTCAC 1013
DB 168 AlaValSerArgAlaPheGlnAspPheGlnLeuLysProGlnValLeuGlnProValThr 187
QY 1014 TCTGTGCCCGACATCAGACGCTGCAGCTGACCCCAATGACAGGTTGATTTGTGGCC 1073
DB 188 AlaGlnProAspValThrSerHisLysIleThrProSerArgGlnPheLeuIleLeuAla 207
QY 1074 TGTGTGGGCTCTTCAAGCTTTACCCCAAGAACCGCGAATTGATCTTGCTCTGT 1133
DB 208 SerAspGlyLeuTyrAspValLeuSerAspGlnGlnValAlaSerIleValArgSerGln 227
QY 1134 CTCGAGATGAAAAGATGTCAGACCCGGAAGGAAAGTCGCGACGCCGCTACGAA 1193
DB 228 LeuSerAspGlyProMetGln----- 234
QY 1194 GCAGCCTGCAACAGGCTGCCCAACAGGCGGTGACGGGCTCGGCGACAAACGTC 1250
DB 235 ---AlaAlaGlnLysLeuValAspTyrAlaIleAlaTyrGlySerGlnAspAsnIle 252

RESULT 5
US-10-171-404A-46
/ Sequence 46, Application US/10171404A
/ GENERAL INFORMATION:
/ APPLICANT: BASF PLANT SCIENCE GMBH
/ TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS II
/ FILE REFERENCE: 16113-0119
/ CURRENT APPLICATION NUMBER: US/10/171,404A
/ PRIOR FILING DATE: 2002-11-19
/ PRIOR APPLICATION NUMBER: 60/295,680
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 46
/ LENGTH: 434
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
US-10-171-404A-46

Alignment Scores:
Pred. No.: 1.14e-15 Length: 434
Score: 353.50 Matches: 125
Percent Similarity: 44.71% Conservative: 65
Best Local Similarity: 29.41% Mismatches: 148
Query Match: 13.81% Indels: 87
DB: 6 Gaps: 19
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US-09-935-124A-1 (1-1422) x US-10-171-404A-46 (1-434)
QY 105 GACCTCTTGGGAGCCTGCGGAGCCCGAGCC---TGGCGGCGCCGCTGCGCGGAAA 161
DB 45 AspleMetValSerLeuProGluThrSerCySerValSerGlySerHisGlySer 64
QY 162 GAAGTCAGAAAAGACCCCTGCTCTTGATGATGACCTCTCCGGGACAGACTGACTCA 221
DB 65 GluSerArgIyValLeuHisSerArgIleAamSerProAamLeuAamMetIyGluSer 84
QY 222 GGATCAGGGGACCTTGCTTTTGATGATCTCCACCCGCTAGACCTGGCGAT----- 275
DB 85 AlaAlaAlaAspIleValValAsp-----IleSerAlaGlyAspGluIle 100
QY 276 TCGAGTCTCTTGCCACATATCCAGATGATGTA---AAGACTGAAGGAAAGAGCA 332
DB 101 AengIySerAspValThrSerGluIyLeuMetIleSerArgThrGlu----- 116
QY 333 AAGAGAAAACCTCCGAGAGAAAGAAATGCGAGAAAGCTTTGGAAAAAGAAATT 392
DB 117 -----SerHisSerLeuPheGluPheIyS--- 124
QY 393 TGTAAAGCTCTTGCTGATCTTTGCTGAGAGGCTATGCTGAGCGGAAAGGTGAG 452
DB 125 -----SerValProLeuIyGlyPheThrSerIleCyS-----GlyArg 137
QY 453 AGGAGAGAGATGACAGATGCCACGTGATCTGACAGCATCAACGAGAGGTGAGCCC 512
DB 138 ArgProGluMetGluAspAla-----ValSerThrIleProArgPheLeuGlnSer 154
QY 513 CCATCGTCCCTCATT-----ACTCGGCTTTCATATTTTGGT 548
DB 155 SerSerGlySerMetLeuAspGlyArgPheAspProGlnSerAlaAlaHisPhePheGly 174
QY 549 GTTTTGGATGACATGAGAGAAATTCGAGCTCAAAATTTGCTGCAGAAATTTGCTCAA 608
DB 175 ValIyAspGlyHisGlyIyGlySerGlnValAlaAenIyCyArgGluArgMetHisLeu 194
QY 609 AACTTAATCAGAAAATTTCCCTAAA-----GGAGATGATACAGT 647
DB 195 AlaLeuAlaGluGluIleAlaIyGluIyPheMetLeuCyAspGlyIyAspThr---Trp 213
QY 648 GTGAGAAAACCGTGAAGAGATGCTTTTGACACTTTCAGACATGACATGAGAAAGATTC 707
DB 214 LeuGluIySerTrp---LysIyAlaLeuPheAamSerPheLeuArgValAspSerGluIle 232
QY 708 CTTAAACAAGCTTCAGCCAGAGACCTGCTCGAAGAGGTGCTGACCTGCCAGTGTGTT 767
DB 233 GluSerValAlaProGluThrVal-----GlySerThrSerValValAla 247
QY 768 CTGCTGTAGACAACATCTTTATATGCTCCAACTCGAGATATGTCGGCAATCTTGCT 827
DB 248 ValValPheProSerHisIlePheValAlaAamCyGlyAspSerArgAlaValLeuCyS 267
QY 828 CGTTATATGAGAGAGTCAAAAACATGACGCTTAAAGCTTCAGCAAGAACATPATCCA 887
DB 268 Arg-----GlyLysThrAlaLeuProLeuSerValAspHisIyAspTrp 281
QY 888 ACTCAGTATGAAGCGAGTGAAGATACAGAAAGCTGAGGAAAGCTC-----AGG 938
DB 282 AspArgGluAspGluAlaAlaArgIleGluAlaAlaGlyIyLysValIleGluTrpAsn 301
QY 939 GATGGCGTCTTTGGCGCTGCTGAGGTGTCACGCTCACTTGGGAGCGGCACTGAAC 998
DB 302 GlyAlaArgValPheGlyValLeuAlaMetSerArgSerIleGlyAsp---ArgTylLeu 320
QY 999 CGCTGGCGTCTCACCTCTGCTGCCGACATCAAGCGTCCGACGTGACCCCAATGACAGG 1058
DB 321 LysProSerIleIleProAspProGluValThrAlaValIyAspArgValIyGluAspAsp 340
QY 1059 TTCATTTTGTGGCTGTGATGGCTCTTCAAGTCTTAACTTAACTCCAGAAAGACCGCTGAC 1118
DB 341 CysLeuIleLeuAlaSerAspGlyValIyTrpAspValMetThrAspGluAlaIyCyGlu 360
QY 1119 TTGATC-----TTGTCC 1130
DB 361 MetAlaArgIyValArgIleLeuLeuIyPheIyLysIyAspAlaValAlaGlyAspAlaSer 380
QY 1131 TGTCTGAGAGATGAAAAGATCCAGACCCGGGAAAGGAAAGTCCGACGCGCCCTTAC 1190
DB 381 LeuLeuAlaAspGluArg-----ArgIyGluGluIyS-----AspProAlaAla 395
QY 1191 GAAGCAGCTTCGACAGGCTGCGACACAGCGCTGACCGGCGCTGCGCCGACAGCTC 1250
DB 396 MetSerAlaAlaGluIyLysLeuSerIyLeuAlaIleGlnArgIySerIyAspPheIle 415
QY 1251 ACTGTAGTGTGTG 1265
DB 416 SerValValValVal 420

RESULT 6
US-10-342-224-78 Application US/10342224
; Sequence 78, Application US/10342224
; GENERAL INFORMATION:
; APPLICANT: Nathalie Verbruggen
; TITLE OF INVENTION: Genes Involved in Tolerance to Environmental Stress
; FILE REFERENCE: CNM-01205
; CURRENT APPLICATION NUMBER: US/10/342,224
; PRIOR FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: US/09/762,154
; PRIOR FILING DATE: 2002-02-02
; PRIOR APPLICATION NUMBER: EP 98202634.6
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-342-224-78

Alignment Scores:
Pred. No.: 1,3e-14 Length: 380
Score: 337.50 Matches: 102
Percent Similarity: 45.30% Conservative: 62
Best Local Similarity: 28.18% Mismatches: 129
Query Match: 13.18% Indels: 69
DB: Gaps: 12

US-09-935-124A-1 (1-1422) x US-10-342-224-78 (1-380)
QY 273 GATTCAGTCTCTTGGCCACATCATATCCAGATGCTAAAG----- 314
DB 19 AspAamThrSerIleAlaThrGluIleAspThrLeuGluAsnLeuAspAspThrArgGln 38
QY 315 ---ACTAAGGAGAAAGAGCAAAAGAAAACCTCCGAGGAAAGAAATGCGAGTGA 371
DB 39 IleSerIyGlyIyAspProProArgHisLeuThrSerSerAlaThrArgLeuGlnLeuAla 58
QY 372 GAGCTGTGAAAAGAAATTTGT-----AAAGCTCT 404
DB 59 AlaAsnAlaAspValAspValCysAsnLeuValMetIySerSerLeuAspAspIySerGlu 78
QY 405 TCGGTATCTTTGCTGTAAGGCTTATGCTGAGCGGAGGAGGTGAGAGAGAGATG 464
DB 79 PheLeuProValIyArgSerIySerCyAlaIu---GlnIyAlaIySerIlePheMet 97
QY 465 CAGATGCCACGTCATCTCTGACAGACATCACCGAGAGGTGATGAGCCCATGCTCCTC 524
DB 98 GluAspGluHisIleIyCysIleAspAspLeuValAsnHisLeuGlyAlaAlaIleGlnCys 117
QY 525 ATTACTGGGTTTCATATTTTGTCTTTTGTATGACATGAGAAATTTGACCTCAGAAA 584
DB 118 SerSerIleuGlyAlaPheIyArgIyValPheAspIyHisIyGlyIyThrAspAlaHis 137

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Oy 585 TTTCGTGCAGCATTTTGCATCAAAATCTTAATAGA-----AAATTCCTTAAGAGAT 638
Db 138 PheValArgIySbAnIleUeUArgPheIleValGIuAbpSerPhePro----- 154
Oy 639 GTAAATCAAGTGAAGAAACCGTAGAAGATGCCCTTTGGACACTTCAAGCATCTGAT 698
Db 155 ---LeuCysValIySlyValIleIyS-----SerIaPheLeuIySAlaIb 169
Oy 699 GAAGAGTTCCTTAACAAGCTCCAGCCGACAAAGCTCGCTCGAAGAAAGATGGCTCCATCC 758
Db 170 TyGluPheIaIaAbpAbpSerSerLeuAbp-----IleSerSerIyIhThrIa 186
Oy 759 ACGTGCTGTCTGCCTGTAGACAACATTTCTTAATATTCGCAACCTCGAGATATGCGGCA 818
Db 187 LeuThrAlaPheIlePheGIyArgArgLeuIleIaIaAbnAlGIyAbpCysArgIa 206
Oy 819 ATCTTGTCGTCTTAATATGAGAGAGTCAAAACATGCAAGCTTTAAGCTTCAGCAAGAG 878
Db 207 ValLeuGIyAyg-----ArgGIyAygAlIleIleUeUeSerIySb 220
Oy 879 CATATCCCAACTCAGTATGAGAGACGAGATGAGATGACAGAAGCTCGAAGAAACCTCAGG 938
Db 221 HleIySProAbnCySthrAlaGIyIyValArgIleGIuIySleuGIyGIyValIyIyr 240
Oy 939 GATGGCGCTGTTTGGCGCTGCTCTAAGAGTGTCAAGCTCCATTTGGGACCGGSCATGACAAG 998
Db 241 AepGIyIyrLeuAbnGIyGIuIeUeSerValAlaIyAlaIleGIyAbpTrhIeMetIyS 260
Oy 999 -----CGCTCGGCGTGCACCTGTGCTCGACCGACGACGCTGCGACGCTG 1043
Db 261 GIyProIySbGIySerAlaCySProIeUeSerProGIuProGIuIeUeInGIyIhThrAbpLeu 280
Oy 1044 ACCCCCAATGACAGCTTCATTTGTGGCTGTGATGGAGCTCTTCAAGCTCTTAACCCCA 1103
Db 281 SerGIuAbpAbpGIuPheIeUleIeMetGIyCyAAbpGIyLeuThrAbpAlaMetSer 300
Oy 1104 GAAGAAGCGCGTAACCTCATCTGTCTGTCTCGAAGATGAAGATCAAGACCGGGAA 1163
Db 301 GIuCyAAbpAlaIhThrIle----- 306
Oy 1164 GGAAGATCCGACGCGGACGCCGCTACGA-----GCAGCTGTC 1202
Db 307 -----AlaArgIySbGIuIeUeMetIleIaAbnAbpProGIuIyArgCyS 320
Oy 1203 AACAGG---CTGGCCACAAGAAGCGGCTGACAGCGGGCTCGAGCCGACAAGCTCACTGTAGT 1259
Db 321 SerIrgIeUeUValArgGIuAlaIeUySArgAbnThrCyAAbpAbnIhThrValIle 340
Oy 1260 GTGGGTG 1265
Db 341 ValVal 342

RESULT 7
US-09-724-676-79624
/ Sequence 79624, Application US/09724676
/ GENERAL INFORMATION:
/ APPLICANT: Compugen LTD
/ TITLE OF INVENTION: Variants of alternative splicing
/ FILE REFERENCE: 129181.4 Compugen
/ CURRENT APPLICATION NUMBER: US/09/724,676
/ NUMBER OF SEQ ID NOS: 97222
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 79624
/ LENGTH: 354
/ TYPE: PRF
/ ORGANISM: Homo sapiens
/ US-09-724-676-79624

```

Alignment Scores:	
Pred.' No.:	1.63e-14
Scores:	336.00
Percent Similarity:	49.00%
Length:	354
Matches:	100
Conservative:	47

Best Local Similarity:	33.33%	Mismatches:	105
Query Match:	13.12%	Indels:	48
DB:	5	Gaps:	12

[illegible]

```

RESULT 8
US-09-124-676-79625
; Sequence 79625, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen

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[illegible][illegible]

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QY 1005 -----GGTGTACC-----TCGTGCCCCGACATCAGA 1031
Db 206 HLeGlyLybGlyProThrGluGlnLeuValSerProGluProGluValHisAspIleGlu 225
QY 1032 CGGTGCAGCTGACCCCAATGACAGTTTCATTTGTGGCCCTGTGATGGGCTTTCAG 1091
Db 226 ArgSerGlu-----GluAspAspGlnPheIleIleLeuValCysAspGlyIleTrpAsp 243
QY 1092 GTCTTTACCCAGAGAGAGCCGTGACTTCATCTGTCTGTCTGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGlnGluLeuGlnCysAspPheValArgSerArgLeuGluValThrAspAsp 263
QY 1146 AAGATCCAGACCCGGAGAGGAAAGTCCGACCCGACCCGTACGAGAGCCTTCCAC 1205
Db 264 -----LeuGluValValCysAsn 269
QY 1206 AGGCTGGCCACAGAGCGGTGACGCGGGCTCGCCGACAGACTCATCTGTGATGGTG 1265
Db 270 GluValValAspThrCysLeuTyrlYsGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 10
US-09-724-676-79627
; Sequence 79627, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79627
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-79627

Alignment Scores:
Pred. No.: 1,63e-14 Length: 354
Score: 336.00 Matches: 100
Percent Similarity: 49.00% Conservative: 47
Best Local Similarity: 33.33% Mismatches: 105
Query Match: 13.12% Indels: 48
DB: Gaps: 12

US-09-935-124A-1 (1-1422) x US-09-724-676-79627 (1-354)
QY 417 GGTCTGAAGGGCTATGTGCTGACGCGAAGGTGAGAGGAGAGATGCAGATGCCAC 476
Db 21 GtyleuArgTyrlYsLeuSerMetGlnGlyTrpArgValGluMetGluAspIleHis 40
QY 477 GTCATCTGTAAGACATCACCGAGAGTGAAGCCCAATCGTCCCTCATTAATCGGGTT 536
Db 41 ThrAlaValIleGlyLeu-----ProSerGlyLeu---GluSerTrp 53
QY 537 TCATATTTTGTCTTTTGTATGAGATGAGAAATTCAGACCTCAAAATTTGCTGCACAG 596
Db 54 SerPhePheAlaValTyrlYsArgGlyHisAlaGlySerGlnValAlaTyrlYsCysGlu 73
QY 597 AATTGTCATCAAACTTAATCAGAAAAATTTCT--AAAGAGAT-----GTATACAGT 647
Db 74 HisLeuLeuAspHisIleThrAsnGlnAspPheGlySerAlaGlyAlaProSer 93
QY 648 GTAGAGAAAAACGTGAAGAGATCCCTTTTGACATTTCAAGATATCTGATGAAGGTTT 707
Db 94 ValGlyL--AsnValYsAsnGlyIleArgTrpGlyPheLeuGluIleAspGlnHisMet 112
QY 708 CTTAAACAGCTTCAGAGAGAGCTGCGCTGGAAGATGGTGCATCGCAGCTGTGTT 767
Db 113 ArgValMetSerGlnTyrlYsValHisGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
QY 768 CTGGCTGTAGACAAATCTTTATATATGCGCAACTCGAGATAGTGGGCAATCTTGTT 827
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Db 133 LeuIleSerProGlnHisThrTyrlYsPheIleAsnCysGlyAspSerArgGlyLeuLeuCys 152
QY 828 CTTATTAATGAGAGAGTCAAAAACATGACAGCTTAAGCCTTGAAGGAAAGCATATATCA 887
Db 153 Arg-----AsnArgYsValHisAspPheThrGlnAspHisIlePro 166
QY 888 ACTCAGATGAAGAGCCGATGAGATGATACAGAGCTGAGAGAAACGTGACGAGTGGCGT 947
Db 167 SerAsnProLeuGlnGluGluArgIleGlnAsnAlaGlyIleSerValMetIleGlnArg 186
QY 948 GTTTGGGCTGTAGAGTGTACAGCTTCATTTGGGAGCGGCACTACAGAGCTTGC--- 1004
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlnAspPheAspTyrlYs---CysVal 205
QY 1005 -----GGTGTACC-----TCGTGCCCCGACATCAGA 1031
Db 206 HLeGlyLybGlyProThrGluGlnLeuValSerProGluProGluValHisAspIleGlu 225
QY 1032 CGGTGCAGCTGACCCCAATGACAGTTTCATTTGTGGCCCTGTGATGGGCTTTCAG 1091
Db 226 ArgSerGlu-----GluAspAspGlnPheIleIleLeuValCysAspGlyIleTrpAsp 243
QY 1092 GTCTTTACCCAGAGAGAGCCGTGACTTCATCTGTCTGTCTGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGlnGluLeuGlnCysAspPheValArgSerArgLeuGluValThrAspAsp 263
QY 1146 AAGATCCAGACCCGGAGAGGAAAGTCCGACCCGACCCGTACGAGAGCCTTCCAC 1205
Db 264 -----LeuGluValValCysAsn 269
QY 1206 AGGCTGGCCACAGAGCGGTGACGCGGGCTCGCCGACAGACTCATCTGTGATGGTG 1265
Db 270 GluValValAspThrCysLeuTyrlYsGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 11
US-09-724-676A-79624
; Sequence 79624, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79624
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-79624

Alignment Scores:
Pred. No.: 1,63e-14 Length: 354
Score: 336.00 Matches: 100
Percent Similarity: 49.00% Conservative: 47
Best Local Similarity: 33.33% Mismatches: 105
Query Match: 13.12% Indels: 48
DB: Gaps: 12

US-09-935-124A-1 (1-1422) x US-09-724-676A-79624 (1-354)
QY 417 GGTCTGAAGGGCTATGTGCTGACGCGAAGGTGAGAGGAGAGATGCAGATGCCAC 476
Db 21 GtyleuArgTyrlYsLeuSerMetGlnGlyTrpArgValGluMetGluAspIleHis 40
QY 477 GTCATCTGTAAGACATCACCGAGAGTGAAGCCCAATCGTCCCTCATTAATCGGGTT 536
Db 41 ThrAlaValIleGlyLeu-----ProSerGlyLeu---GluSerTrp 53
QY 537 TCATATTTTGTCTTTTGTATGAGATGAGAAATTCAGACCTCAAAATTTGCTGCACAG 596
Db 54 SerPhePheAlaValTyrlYsArgGlyHisAlaGlySerGlnValAlaTyrlYsCysGlu 73
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QY 597 AATTGCATCAAACTTAATCAAAAATTTCCT---AAGAGAT-----GTATCACT 647
DB 74 H1sleuEunaphis1lethrAenandlnaphrhelelyserAlaGlyAlaProser 93
QY 648 GTAGAGAAAACCGTGAAGAGATCGCTTTTGACACTTTCACGATATCGATGAAGATTC 707
DB 94 ValGlu---AsnValIysasnGlyIleArgThrGlyPheleuGluIleAspGlnH1smeC 112
QY 708 CTTAAACAGCTTCACGACGAGGCTCGTGAAGATGGGTCACTGCCACCTGTGTT 767
DB 113 ArgValmeSerGluIlyserH1sleGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
QY 768 CTGGCTGTGACAAACATCTTATATTCGCAACCTCGAGATGTGCGGCAATCTGTGT 827
DB 133 LeuIleSerProGlnH1sThrGlyPheIleHnCyseGlyAspSerThrGlyLeuLeuCyS 152
QY 828 CGTATATATGAGAGAGTCMAAAACATGACGCTTAAGCTCAGCAAAAGACATATATCA 887
DB 153 Arg-----AsnArgIySerValH1sPhePheThrGlnAspH1sLeuPro 166
QY 888 ACTCAGATAGAGAGCGGATGAGATACAGAAAGCTGCGAGAAACGTACAGGATGGGCGT 947
DB 167 SerAsnProleuGlnIlyserGluArgIleGlnAsnH1sleGlyIlySerValmeCilleGlnArg 186
QY 948 GTTTGGGCGCTGTAAGGTGTCACTGCTCCATTTGGGAGCGGACGAGTACAGCGCTGC-- 1004
DB 187 ValAsnGlySerleuH1sleValSerArgAlaIleuGlyAspPheAspTyrIys---CysVal 205
QY 1005 -----GGTGTCAAC-----TCTGTCCCGACATGCA 1031
DB 206 H1sGlyIyserGlyProThrGlnIleuValSerProGluProGluValH1sAspIleGlu 225
QY 1032 CGCTGCGACGTGACCCCAATGACAGTTCAATTTGTGGCTGTGATGGGCTGTCAAG 1091
DB 226 ArgSerGlu-----GluAspAspGlnPheIleIleleuH1sCysAspGlyIleTyrAsp 243
QY 1092 GTCTTACCCCAAGAAAGCCGTAATCTTCCTGTCGCTCGTCAAG-----GATGAA 1145
DB 244 ValmeGlyAsnGlnIleuLeuCyAspPheValArgSerArgIleuGlnValThrAspAsp 263
QY 1146 AAGATCCAGACCCGGAGAGGAAAGTCCGACGCGACGCCCGCTACAGACGCTGCAAC 1205
DB 264 -----GGTGTCAAC-----LeuGlnIlySerValCysAsn 269
QY 1206 AGGCTGCGCAACAGCGGTGACGCGGGCTCGCGCGACACGTCACGTGATGTGTG 1265
DB 270 GluValValAspHrCysleuTyrIyserGlySerArgAspAsnmeSerValIleleuIle 289

RESULT 12
; Sequence 79625, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79625
; LENGTH: 354
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-724-676A-79625

Alignment Scores:
Pred. No.: 1,63e-14 Length: 354
Score: 336.00 Matches: 100
Percent Similarity: 48.00% Mismatches: 47
Best Local Similarity: 33.33% Indels: 105
Query Match: 13.12% Gaps: 12
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US-09-935-124a-1 (1-1422) x US-09-724-676A-79625 (1-354)
QY 417 GGTCTGAAGGCTATGCTGAGCGGAAAGGTGAGGAGGAGATGCAAGATCCCAAC 476
DB 21 G1yleuArgTyrG1yleuSerSermeGlnGlyTyrArgValGlnIleGlnIleAspH1s 40
QY 477 GTCATCTCTCAACAGCACTTCAACCGAGAGTGTAGGCCCCCATCTGCTCCATTACTCGGGTT 536
DB 41 ThrAlaValIleGlyLeu-----ProserGlyLeu---GluSerTyr 53
QY 537 TCAATTTTCTGTGTTTGTATGATGACATGAGAAATTCGACCTCAAAATTTCTGCAAG 596
DB 54 SerPhePheAlaValTyrAspGlyH1sAlaGlySerGlnValAlaIySerCysCysGlu 73
QY 597 AATTGCATCAAACTTAATCAAAAATTTCCT---AAGAGAT-----GTATCACT 647
DB 74 H1sleuEunaphis1lethrAenandlnaphrhelelyserAlaGlyAlaProser 93
QY 648 GTAGAGAAAACCGTGAAGAGATCGCTTTTGACACTTTCACGATATCGATGAAGATTC 707
DB 94 ValGlu---AsnValIysasnGlyIleArgThrGlyPheleuGluIleAspGlnH1smeC 112
QY 708 CTTAAACAGCTTCACGACGAGGCTCGTGAAGATGGGTCACTGCCACCTGTGTT 767
DB 113 ArgValmeSerGluIlyserH1sleGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
QY 768 CTGGCTGTGACAAACATCTTATATTCGCAACCTCGAGATGTGCGGCAATCTGTGT 827
DB 133 LeuIleSerProGlnH1sThrGlyPheIleHnCyseGlyAspSerThrGlyLeuLeuCyS 152
QY 828 CGTATATATGAGAGAGTCMAAAACATGACGCTTAAGCTCAGCAAAAGACATATATCA 887
DB 153 Arg-----AsnArgIySerValH1sPhePheThrGlnAspH1sLeuPro 166
QY 888 ACTCAGATAGAGAGCGGATGAGATACAGAAAGCTGCGAGAAACGTACAGGATGGGCGT 947
DB 167 SerAsnProleuGlnIlyserGluArgIleGlnAsnH1sleGlyIlySerValmeCilleGlnArg 186
QY 948 GTTTGGGCGCTGTAAGGTGTCACTGCTCCATTTGGGAGCGGACGAGTACAGCGCTGC-- 1004
DB 187 ValAsnGlySerleuH1sleValSerArgAlaIleuGlyAspPheAspTyrIys---CysVal 205
QY 1005 -----GGTGTCAAC-----TCTGTCCCGACATGCA 1031
DB 206 H1sGlyIyserGlyProThrGlnIleuValSerProGluProGluValH1sAspIleGlu 225
QY 1032 CGCTGCGACGTGACCCCAATGACAGTTCAATTTGTGGCTGTGATGGGCTGTCAAG 1091
DB 226 ArgSerGlu-----GluAspAspGlnPheIleIleleuH1sCysAspGlyIleTyrAsp 243
QY 1092 GTCTTACCCCAAGAAAGCCGTAATCTTCCTGTCGCTCGTCAAG-----GATGAA 1145
DB 244 ValmeGlyAsnGlnIleuLeuCyAspPheValArgSerArgIleuGlnValThrAspAsp 263
QY 1146 AAGATCCAGACCCGGAGAGGAAAGTCCGACGCGACGCCCGCTACAGACGCTGCAAC 1205
DB 264 -----GGTGTCAAC-----LeuGlnIlySerValCysAsn 269
QY 1206 AGGCTGCGCAACAGCGGTGACGCGGGCTCGCGCGACACGTCACGTGATGTGTG 1265
DB 270 GluValValAspHrCysleuTyrIyserGlySerArgAspAsnmeSerValIleleuIle 289

RESULT 13
; Sequence 79626, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; NUMBER OF SEQ ID NOS: 97222
```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79626
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-79626

Alignment Scores:
Pred. No.: 1,63e-14      Length: 354
Score: 336.00           Matches: 100
Percent Similarity: 49.00% Conservative: 47
Best Local Similarity: 33.33% Mismatches: 105
Query Match: 13.12%      Indels: 48
DB: 5                   Gaps: 12

US-09-935-124A-1 (1-1422) x US-09-724-676A-79626 (1-354)

QY 417 GGTCTGAAGGCTATGCTGGCTGAGCGGAGGCTGAGAGGAGATGCAAGATGCCAC 476
DB 21 Gtyleuargtgclyleusersetmetglnlytpragvalglmetgluaapralahs 40
QY 477 GTGATCTGAACGACATCACCAGAGGTGAGGCCCTGCTCCCTCATTACTCGGGTT 536
DB 41 ThrAlaValIleGlyLeu-----ProserGlyLeu---GluserTpr 53
QY 537 TCATATTTGCTGTTTGTGATGACATGAGAGAAATTCGAACCTCAAAATTTGTCACAG 596
DB 54 SerphehelaValtyrghlyserglnhlaaglyserglnvalahlytyrcysgln 73
QY 597 AATTGTCATCAAACTTAATCAGAAAATTTCT--AAAGAGAT-----GTAACTAGT 647
DB 74 HleleuleuAphriIlethraAasnGlnAapPhehyseglYserAlaGlyAlaProser 93
QY 648 GTAGAGAAAACCGTGAAGAGATGCTTTTGACACTTTCAGACATCTGATGAAGAGTTTC 707
DB 94 ValGlu---AenValIyvaenGlyIleargThrglyPheleugluIleapGlnhIsmet 112
QY 708 CTTAAACAACTTCACAGCAAGAGCTGCTGGAAGATGGTCACTGCCAGCTGTGT 767
DB 113 ArgValmetserGlnlyyehniAglYAlaAparaserGlyserThraIaValGlyVal 132
QY 768 CTGGGCTGACAAACATTTCTTTATTTGSCAACTCGAGATAGTGGGCAATCTGTGT 827
DB 133 LeuIleserProGlnIethrtyrPheIleAenCyseglYAspserkrglyLeuleuCy 152
QY 828 CGTTATGATGAGAGAGTCAAAAACATGACGCTTAAGCCTCAAGCAAGCATTAATCCA 887
DB 153 Arg-----AenArgIyvaIlnIerPhehethrGlnAapRhslyPro 166
QY 888 ACTCAGTATGAGAGCGGATGAGATACAGAAAGCTGAGAAAAGTCAAGGATGGCGCT 947
DB 167 SerAapProleuglnlyyehniAglYAlaAparaserGlyserThraIaValGlyVal 186
QY 948 GTTTGGGCTGACAGGCTGACAGCTCCATTGGGAGCGGCACTGACAAAGCCTGC--- 1004
DB 187 ValAenGlySerleuAlaValiserArgAlaIleuglyAapPheAapTyrlYs---CyVal 205
QY 1005 -----GGTGTCAAC-----TCTGTGCCCGCATCAGA 1031
DB 206 HieGlyLyseGlyProthrglnGlnLeuValSerProGlnProGlnValhIaapRhslyPro 225
QY 1032 CGCTGCAGCTGACCCCAATGACAGATTCATTTGCTGCTGATGAGGCTTCCTCAAG 1091
DB 226 ArgserGlu-----GluAapRaglnPheIleIleuAlaCyvaapRgylIletrAap 243
QY 1092 GTCTTTAATCCCAAGAAAGCGGTGAACCTTGTCTGTCTCGAG-----GATGAA 1145
DB 244 ValmetGlyAasnGlyyehniAglYAlaAparaserGlnhIaValThraAapR 263
QY 1146 AATATCCAGACCCGGGAAGGAAGTCCGACGCGGCTACAGAAAGCTTCGAAC 1205
DB 264 -----GGTGTCAAC-----LeuGlnlyyValCyvaap 269

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QY 1206 AGCTGGCCAAAGCGGCTGACGCGGCTCGCCCAACGTCATGTGATGCTGTG 1265
DB 270 GluValIaAapRhslyserGlnhIaAparaserGlnhIaAparaserValIleuLeu 289

RESULT 14
US-09-724-676A-79627
; Sequence 79627, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724.676A
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79627
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-79627

Alignment Scores:
Pred. No.: 1,63e-14      Length: 354
Score: 336.00           Matches: 100
Percent Similarity: 49.00% Conservative: 47
Best Local Similarity: 33.33% Mismatches: 105
Query Match: 13.12%      Indels: 48
DB: 5                   Gaps: 12

US-09-935-124A-1 (1-1422) x US-09-724-676A-79627 (1-354)

QY 417 GGTCTGAAGGCTATGCTGGCTGAGCGGAGGCTGAGAGGAGATGCAAGATGCCAC 476
DB 21 Gtyleuargtgclyleusersetmetglnlytpragvalglmetgluaapralahs 40
QY 477 GTGATCTGAACGACATCACCAGAGGTGAGGCCCTGCTCCCTCATTACTCGGGTT 536
DB 41 ThrAlaValIleGlyLeu-----ProserGlyLeu---GluserTpr 53
QY 537 TCATATTTGCTGTTTGTGATGACATGAGAGAAATTCGAACCTCAAAATTTGTCACAG 596
DB 54 SerphehelaValtyrghlyserglnhlaaglyserglnvalahlytyrcysgln 73
QY 597 AATTGTCATCAAACTTAATCAGAAAATTTCT--AAAGAGAT-----GTAACTAGT 647
DB 74 HleleuleuAphriIlethraAasnGlnAapPhehyseglYserAlaGlyAlaProser 93
QY 648 GTAGAGAAAACCGTGAAGAGATGCTTTTGACACTTTCAGACATCTGATGAAGAGTTTC 707
DB 94 ValGlu---AenValIyvaenGlyIleargThrglyPheleugluIleapGlnhIsmet 112
QY 708 CTTAAACAACTTCACAGCAAGAGCTGCTGGAAGATGGTCACTGCCAGCTGTGT 767
DB 113 ArgValmetserGlnlyyehniAglYAlaAparaserGlyserThraIaValGlyVal 132
QY 768 CTGGGCTGACAAACATTTCTTTATTTGSCAACTCGAGATAGTGGGCAATCTGTGT 827
DB 133 LeuIleserProGlnIethrtyrPheIleAenCyseglYAspserkrglyLeuleuCy 152
QY 828 CGTTATGATGAGAGAGTCAAAAACATGACGCTTAAGCCTCAAGCAAGCATTAATCCA 887
DB 153 Arg-----AenArgIyvaIlnIerPhehethrGlnAapRhslyPro 166
QY 888 ACTCAGTATGAGAGCGGATGAGATACAGAAAGCTGAGAAAAGTCAAGGATGGCGCT 947
DB 167 SerAapProleuglnlyyehniAglYAlaAparaserGlyserThraIaValGlyVal 186
QY 948 GTTTGGGCTGACAGGCTGACAGCTCCATTGGGAGCGGCACTGACAAAGCCTGC--- 1004
DB 187 ValAenGlySerleuAlaValiserArgAlaIleuglyAapPheAapTyrlYs---CyVal 205
QY 1005 -----GGTGTCAAC-----TCTGTGCCCGCATCAGA 1031

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Db 206 HieglylyglyprothrgluInleuValserProgluVal1Hisaprlleglu 225
QY 1032 CGGTGGCACTGACCCCAATGACAGCTTCATTTGGCTGTGATGGCTCTCAAG 1091
Db 226 Ariserglu-----GluaspgrglnPhilelleleuAlaCyaspgrgylletrparp 243
QY 1092 GTCTTTACCCCAAGAAAGCCGTGAATCTTCTGTCTGTCTGAG-----GATGAA 1145
Db 244 ValMetGlyAsnGluGluLeuCyaspPheValArgSerArgLeuGluValThrAspAsp 263
QY 1146 AGATCCAGACCCGGGAAAGGAGAGTCCGACGCCGCTACAGAACGACCTGCAC 1205
Db 264 -----LeuGluValCysAsn 269
QY 1206 AGCTGGCCACAGACGCTGACGCGGCTCGCCGACACGTCACTGTGATGTGTG 1265
Db 270 GluValValAspThrCysLeuTyrlglySerArgAspAsnMetSerValIleLeuIle 289

RESULT 15
US-10-168-506-21
; Sequence 21, Application US/10168506
; GENERAL INFORMATION:
; APPLICANT: PLOMAN, GREGORY D.
; APPLICANT: MARTINEZ, RICARDO
; APPLICANT: WATTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDASANAM, SUCHA
; APPLICANT: HILL, RON
; APPLICANT: FLANAGAN, PETER
; TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
; FILE REFERENCE: 038602/1351
; CURRENT APPLICATION NUMBER: US/10/168, 506
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: PCT/US00/34736
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-506-21

Alignment Scores:
Pred. No.: 4,08e-14 Length: 360
Score: 330.00 Matches: 99
Percent Similarity: 47.63% Conservative: 62
Best Local Similarity: 29.29% Mismatches: 117
Query Match: 12.89% Indels: 60
DB: Gaps: 13

US-09-935-124a-1 (1-1422) x US-10-168-506-21 (1-360)
QY 303 CAGATGTTAAAGCTGAAGGAAAGGCAAGAAAGAACTCCGACGAGAGAAAGAT 362
Db 57 LysMetValIysSerIys-----ValAlaGluThrMetGlnAsnAspArgLeu 72
QY 363 GGCAGTGAAGAGCTTGTGAAAGAAAGTTGTAAAGCTCTTCGTGATCTTGGTGTG 422
Db 73 GlyGlyLeuAspValLeuGluAlaGluPheSerIysThr-----TyrIuPhe 88
QY 422 AAGGCTAT-----GTGCTGACGCGAAGGCTGAGAGGAGAGATGACAGATGCC 473
Db 89 LysAsnHisAsnValAlaValItyrSerIleGlnGlyArgArgAspHisMetGluAspArg 108
QY 474 CAGCTCATCTGACGACATCACCGAGGAGTGAAGCCCGCCATCGCTCATTTCTCGG 533
Db 109 PheGluValIleThrAspLeuAlaAsnLysThrHisPro-----TyrIuPhe 121
QY 534 GTTTCATATTTTGTCTGTTTGTGATGAGATGAGAGATGAGAGCTCAAAATTTGTGCA 593
Db 122 ---SetIlePheGlyIlePheAspGlyHisGlyGluThrAlaAlaGluTyrValLys 140

QY 594 CAGAAATTTG-----CATCAAACTTAATCAGAAATTTCTTAAGCA 635
Db 141 SerArgLeuProGluAlaLeuLysGlnHisLeuGlnAspTyrGluLysAspLysGluAsn 160
QY 636 GATGTATCATGATGATGAGAAACCGTGAAGATGCTTTTGGACACTTTCAGACATCT 695
Db 161 SerValLeuSerTyrGlnThrIleLeuGluGlnGlnIleLeuSer-----Ile 176
QY 696 GATGAAGAGTCTTAAACAGCTTCACAGCAGAAAGCTGCTGAAAGATGGGTCCACT 755
Db 177 AspArgGluMetLeuGluLysLeuThrValSer-----TyrAspGluAlaGly 192
QY 756 GCCAGGTGCTCTGCTGTA-----GACAACTTTTATATTCGCAACTCGAGAT 809
Db 193 ThrThrCysLeuIleAlaLeuLeuSerAspLysAspLeuThrValAlaAsnValGlyAsp 212
QY 810 AGTCGGCAATCTTGTCTGCTTAATTAAGAGAGAGTCAAAACATGACGCTTAAAGCTTC 869
Db 213 SerArgGlyValLeuCys-----AspLysAspGlyAsnAlaIleProLeu 227
QY 870 AGCAAAAGCATATTCCACTGATGAAGACCGGATGAGATTCAGAAAGCTCGACGA 929
Db 228 SerHisAspHisLysAspTyrGlnLeuLysGluArgLysArgLysArgAlaGlyGly 247
QY 930 AACGTCCAG-----GATGGCGGTGTTTGGGCTGTAGAGTGTCACTCCATT 980
Db 248 PheIleSerPheAsnGlySerTyrArgValGlnGlyIleLeuAlaMetSerArgSerLeu 267
QY 981 GGGAGCGGAGATACAGAGCGCTGCGGTGTACCC-----TCTGTCCCGACATCAGACGTGC 1037
Db 268 GlyAspArgProLeuLysAsnLeuAsnValIleAspAspArgAspIleLeuThrPhe 287
QY 1038 CAGCTGACCCCC---AATGACAGGTTCATTTTGTGAGCTGTGATGGCTTTCAGATC 1094
Db 288 AspLeuAspLysLeuGlnProGluIlePheMetIleLeuAlaSerAspGlyLeuTyrAspAla 307
QY 1095 TTTAACCCCAAGAAAGCCGTGAACCTGATCTGTGCTGCTGAGATGAGAAATATCAG 1154
Db 308 PheSerAsnGluGluAlaValArgPheIleLysGluLysLeuAspGluProHisPheGly 327
QY 1155 ACCCGGAAAGGAAATCCCGACCGACGCGCCGCTACGAAACAGCTCGACAGGCTGGCC 1214
Db 328 AlaLysSer-----IleVal 332

QY 1215 AACAAAGCGGTGACAGCGGCTCTGCGCCGACACGTCACTGTGATGTGTGCGG 1268
Db 333 LeuGlnSerPheTyrArgGlyCyaspProAspAsnIleThrValMetValValLys 350

RESULT 16
US-10-311-764-1
; Sequence 1, Application US/10311764
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.
; APPLICANT: BAUGHN, Mariah R.; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.
; APPLICANT: GRIFFIN, Jennifer A.; HAPALIA, April J.A.
; APPLICANT: KEARNEY, Liam; LEE, Ernestine A.
; APPLICANT: LU Van; NGUYEN, Daniel B.
; APPLICANT: ARVIZO, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom
; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.
; APPLICANT: CHAMLA, Nardine K.; YU, Henry
; APPLICANT: YAO, Monique G.; YU, Henry
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0126 USN
; CURRENT APPLICATION NUMBER: US/10/311,764
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19442
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/212,447
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/213,746
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# PRIOR FILING DATE: 2000-06-22
# PRIOR APPLICATION NUMBER: US 60/215,210
# PRIOR FILING DATE: 2000-06-29
# PRIOR APPLICATION NUMBER: US 60/216,529
# PRIOR FILING DATE: 2000-07-06
# PRIOR APPLICATION NUMBER: US 60/218,080
# PRIOR FILING DATE: 2000-07-12
# PRIOR APPLICATION NUMBER: US 60/220,117
# PRIOR FILING DATE: 2000-07-21
# NUMBER OF SEQ ID NOS: 18
# SOFTWARE: PERL Program
# SEQ ID NO 1
# LENGTH: 372
# TYPE: PR1
# ORGANISM: Homo sapiens
# FEATURE:
# NAME/KEY: misc feature
# OTHER INFORMATION: Incyte ID No: 8124196CD1
US-10-311-764-1

```

Alignment Scores:	
Pred. No.:	2.99e-13
Score:	317.00
Percent Similarity:	41.32%
Best Local Similarity:	27.38%
Query Match:	12.38%
DB:	6
Length:	372
Matches:	112
Conservative:	57
Mismatches:	120
Indels:	114
Gaps:	15

US-09-935-124A-1 (1-1422) x US-10-311-764-1 (1-372)

Oy	180	CTGCTCTTTGATGAC-----CTCCCTCCGGCAGCACTACTGACTCA-----	222
Db	27	LeuLeuGlnAerPheParArgValThrProHicrCyshAsSerSerThrSergLupProArg	46
Oy	222	-----GGATCAGGCGGACCTTGTCTTTTGATGAT-----	253
Db	47	CysSerArgPheAerProAspGlySergLysErgProAlaThrTrpAspAenPheGlyLe	66
Oy	252	-----CTCCACCCCGCTACAGATGGCGGACTCAGGT	281
Db	67	TrpAspAenArgLLeAerGluProLLeuLeuPProPserIle-----	81
Oy	282	TCTCTTGGCACATCAATATCCAGATGGTAAAGACTGAGGGAAGAGCAAGAGAAA	343
Db	81	-----	81
Oy	342	ACCTCCGAGGAAGACAGAAATGGCAGTGAAGACTTGTGAAAAGAAATTGTAAGCC	401
Db	82	-----LysTyrGly-----LysProLLeProLysIle	90
Oy	402	TCTTCGTGATCTTTGGCTGAGAGGGCTATGGCTGACGGGAAAGGGTGAAGGGAGAG	461
Db	91	SerLeuGlnAenValGlyCyshAsSerGlnIleGlyLysAerGlyS--GluAenGluAerP	109
Oy	462	ATGCAGATGCCCAAGCTATCCTGAACGACATCAACGAGAGTGAAGCCCCCATCTCC	521
Db	110	ArgPheAer-----PheAlaGlnLeuThrAerGlu-----	119
Oy	522	CTCATTACTCCGGGTTCATATTGTTGCTGTTTGTATGACATGAGAGAAATTCAGCTCA	581
Db	120	-----ValLeuTyrPheAlaValAlaValArgPheGlyAspGlyGlyProAlaAlaAla	135
Oy	582	AAATTTGCTGACAGAAATTTGATCATCAAAACTTAATCAAGAAATTTCTTAAGAGAGATGA	641
Db	136	AerPheCyshAerThrHicrMetGluLysErgValLeuMetAerLysLeuProLys	152
Oy	642	ATCAGTGAAGAAAACCTGAAGAGATGCTTTTGGACACTTTCAAAGCATCTGATGAA	701
Db	153	-----GluTyrAenLeuGluThrLeuLeuThrLeuAlaPheLeuGluLLeAerLys	169
Oy	702	GAGTTCCTTAAACAAGCT-----TTCAGCCGAGAAAGCTGCTGGAAAGATGGTCCACT	755
Db	170	AlaPheSerSerHicrAlaArgLeuSerAlaAerAlaThrLeuLeuThrSergLysThrThr	189

Oy	756	GCCAGCGTGTCTGGGTCATGACCAACT---	CTTAATTGCCAACTCGGAATAGT	812
Db	190	AlatrhValAlaleueuaagbaeglyllleqlueValalServalaleuysper		209
Oy	813	CGGGCAATCTTGTCGTTAATAGAGAGTCAAAA	CATGCAGCCTTAAGCTCAC	872
Db	210	ArglalleucCyabg-----	LyeGlyLysProMetLysLeuthr	223
Oy	873	AAGAAGCATTAATCCAACCTAGCTTGAAGCGGATGAGATACAGAAGCTGAGAGA---		929
Db	224	IleaphisthrProgluaGlybaerGilyuvgIuarGiletyalyeGelyylphe		243
Oy	930	-----AACGTCAGAGTAGGGCGGTTTTGGGCGTCTAGAGGTGCAGCTCC		977
Db	244	ValAlatrpaenserleuglnPronhisvalaenGlyAryleuAlamechrtrsger		263
Oy	978	ATTGGGAGCGGAGACAGACAGCCGTCGAGTCACTCTGTGSCCSGACATCAGAGCTGC		1037
Db	264	IlecllyapreuparpleuysthrserGlyValllealgluProglutThrLyargtle		283
Oy	1038	CAGTGT---ACCCCATGTCAGGTTCAATTTGTGTGGCTGTGATGGGCTTCAAGTC		1099
Db	284	LysleuhishiIsalaasphaSerPhelauValleuthrThAsrglylleasnhet		303
Oy	1095	TTTACCACAGAGAGAGCGCGTTCATCTTGTCCTGTCTCGAGAGATGMAAGATCCAG		1154
Db	304	ValanserInetnulleCybaephavalanGlnCyhiAepProksnlu-----		321
Oy	1155	ACCCGGAGAGGAAGTCCGACGCCAGCGCCGCTACGAAGACGCTCAACAGGCTGGCC		1214
Db	322	-----	AlalahiValthr	327
Oy	1215	AACAAGCGGTGACGCGGCGTCCGCCGACACATCTCATCTGTATGTGTGCGGATAAG		1274
Db	328	GludlnmalleglnyryglynmrlguaasphaserThralaValaValaProbhegly		347
Oy	1275	CAC TGAGGGGTGCGCGCGCGGCGCAGAG		1301
Db	348	AlatrplystYrLysasnserrlu		356
 RESULT 17 US-09-724-676-80004 ; Sequence 80004, Application US/09724676 ; GENERAL INFORMATION: ; APPLICANT: Compugen LTD ; TITLE OR INVENTION: Variants of alternative splicing ; FILE REFERENCE: 129181.4 Compugen ; CURRENT APPLICATION NUMBER: US/09/724,676 ; CURRENT FILING DATE: 2000-11-28 ; NUMBER OF SEQ ID NOS: 97222 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO 80004 ; LENGTH: 327 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-724-676-80004				
 Alignment Scores: Pred. No.: 5,46e-13 Length: 327 Score: 313.00 Matches: 94 Percent Similarity: 44.65% Conservative: 52 Best Local Similarity: 28.75% Mismatches: 125 Query Match: 12.23% Indels: 56 DB: Gaps: 8				
Oy	US-09-935-124A-1 (1-1422)	x	US-09-724-676-80004 (1-327)	
Oy	333	AAGAGAAAACTCCGAGGAGAGAGATGCGAGTGAAGAGACTGTGGAAAAAGAAATT		392
Db	7	LysEprolyshmrGtulyshIsamAlahisGLyAlaGlyAsn-----		20
Oy	393	TGTAAAGCTCTTCGGTGATCTTTGGTCTGAAGGGCTATGTGGCTGACGGAGGGTGAG		452

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Db 21 -----GlyLeuAArgTyrGlyLeuSerSerMetGlnGlyTyr 32
Oy 453 AGGAGAGAGATGCAGATGCCCACTGCATCAAGCAACGACATCCAGAGAGATGTAAGGCC 512
Db 33 ArgValAGlMetGluSerAlaHisSerTrpAlaValAlaGlyLe----- 46
Oy 513 CCATGCTCCCTCATTAATCCGGGTTTCAATTTTGGCTGTTTGAATGGAATGAGAGATT 572
Db 47 ProHieGlyLeu--GluAerPTPserPhePheAlaValAlaTyrSerHisAlaGlySer 65
Oy 573 CGAGCTCAAAATTTGCTGCAAGAAATTGCATCAAAATCTTAATCAGA----- 620
Db 66 ArgValAlaAsnTyrCysSerTrpHisLeuLeuGlnHisIleThrThrAsnGluAerPhe 85
Oy 621 -----AAATTTCTTAAAGAGATGTAATCACTGATGAGAAAACCTGAGAGA 668
Db 86 ArgAlaAlaGlyLysSerGlySerAlaLeuGlnLeuSerValGlu--AsnAllyAsn 104
Oy 669 TGCCTTTGAGACATTTCAACACTACTGATGAAGAGTTCTCTTAAACAAGCTTCCAGCCAG 728
Db 105 GlyTlIeArgThGlyPheLeuLysValLeaerGlnTyrMetCArgAsnPheSerAerPheLys 124
Oy 729 AAGCTGCGCTGGAAGAAATGGGTCATCGCCAGCTGATGTTCTGGCTGTAGACAACATTTCT 788
Db 125 AsnGlyMetAerAerAerSerGlySerThrAlaValAlaGlyValMetIleSerProLysHisIle 144
Oy 789 TATATTTGCCACCTGGAGAGATAGTGGGGAATCTTGCTGTCCTTAAATGAGAGATGACA 848
Db 145 TyrPheHisGlyLysSerSerArgAlaValLeuTyrAlaGluAsnGlyGln----- 161
Oy 849 AAACATGACCGCTTAAAGCTCAGCAAGAAAGCACTAAATTCACAATCAGTATGAAGAGGATG 908
Db 162 -----ValCyPheSerThrGlnAerHisLysProCysAerProLysGlnLysGlu 178
Oy 909 AGCATACAGAAAGCTGAGAGAAACCTCAAGGATCGGCGCTTTTGGCGCTGTAGAGAGTG 968
Db 179 ArgIleGlnAsnAlaGlyLysSerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
Oy 969 TCACGCTTCATTTGGGAGCGGAGAGTACCAAGCGCTGGCGT----- 1007
Db 199 SerArgAlaLeuHisLysPyrAerPyrLysCysValAerPylLysGlyProThrGlnGln 218
Oy 1008 ---GTCACTCTGTGCGCGACATCCAGACGCTGCACCTGACCCCAATGACAGTTCAATT 1064
Db 219 LeuAlaSerProGlnProGlnValTyrGlnIleLeuArgAlaGlnGluAerGlnPheIle 238
Oy 1065 TTGTGTGACCTGTGATGGCTCTTTCACAGGTCCTTATCCCAAGAAAGACCGTGAATTCATC 1124
Db 235 IleLeuAlaCysAerPylIleTyrAerValMetSerAerGlnGlnLeuGlyGlyTyrVal 258
Oy 1125 TTGTCTCTGTCCAGAGATGAAGAATTCAGACCCCGGAAAGGAGTCCGACGCGAGGCC 1184
Db 259 LysSerAerGlnGlu-----ValSerAerP 266
Oy 1185 CGCTTACAGAAAGAGCTGTCAACAAGCTGCGCAACAAGGCGGTGTCAGCGGCTCGGCGAC 1244
Db 267 AarPheGlnAerValCysAerTrpAlaValAerPheCysLeuHisLysGlyLysSerAerAer 286
Oy 1245 AACGTCACTGTGAGAGGTGGTG 1265
Db 287 AarMetSerIleValLeuVal 293

RESULT 18
US-09-724-676A-80004
Sequence 80004, Application US/09724676A
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLES OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676A
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222

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[illegible]

```
Oy 1125 TTGTCCTGTCGAGAGTAAAGATCCAGACCCGGAGGAGAACTCCGACCCGACGCC 1184
    |||
    |||
Db 259 LysSerArgLeuGlu-----ValSerAsp 266
Oy 1185 CGCTACGAAGCAGCCTCGCAACAGCGTCGCCAACAGGCGGTGACGGGGCTCGGCCGAC 1244
    |||
    |||
Db 267 AspleuGluAsnValCyAsnTrpValValAspThrCysLeuHisIleuSglYserItrAsp 286
Oy 1245 AACGTCACTGTGATGGTGGTG 1265
    |||
    |||
Db 287 AsnMetSerIleValLeuVal 293

RESULT 19
US-09-724-676-80002
; Sequence 80002, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-26
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80002
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-80002

Alignment Scores:
Pred. No.: 5,5e-13 Length: 387
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
DB: Gaps: 8

US-09-935-124A-1 (1-1422) x US-09-724-676-80002 (1-387)
Oy 333 AAGAGAAAACCTCGAGAGAGAAAGATGCGACGTGAGAGACTTGTGGAAAAGAAATT 392
    |||
    |||
Db 7 LysProlYstHnGluYstHnIleAsnAlaHisGlyAlaGlyAsn----- 20
Oy 393 TGTAAAGCCTCTTCGGTATCTTGGTGTGAAGGCGCTATGCGTCAAGCGGAAGGTGAG 452
    |||
    |||
Db 21 -----GlyLeuArgTyrGlyLeuSerSerMetGlnIYTrp 32
Oy 453 AGGAGAGATGACAGATGCCACGTCACTCTGAACGACATCAACGAGAGGTGAAGCCC 512
    |||
    |||
Db 33 ArgValAlaGluMetGluAspAlaHisIstHraIaValAlaGlyIle----- 46
Oy 513 CCATGTCCTCCATTAAGTGGGTTTCATATTTGGCTTTTGTGAGAGATGAGAAATT 572
    |||
    |||
Db 47 ProHisGlyLeu--GluAspTrpSerPhePheAlaValIYTrAspDlYHisIleGlySer 65
Oy 573 CGAGCCTCAAAATTTGCTGCACAGAAATTTGCATCAAAACTTAATCAGA----- 620
    |||
    |||
Db 66 ArgValAlaAsnTrpCysSerThrHisIleLeuGluHisIleThrThrAsnGluAspPhe 85
Oy 621 -----AAATTTCTAAAGAGATGTAAATCAGTGAAGAAAACGTGAAGAGA 668
    |||
    |||
Db 86 ArgAlaAlaGlyLysSerGlySerAlaLeuGluLeuSerValGlu--AsnValIYstAsn 104
Oy 669 TGCCTTTTGGACATTTCAAGCATCTGTGAAGATTCCTTAAACAACTTCCAGCCAG 728
    |||
    |||
Db 105 GlyIleAsnTrpGlyPheLeuYstHnIleAspGluTyrMetArgAsnPheSerAspLeuArg 124
Oy 729 AAGCCTGCTGGAAAGATGGTCACTGCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCT 788
    |||
    |||
Db 125 AsnGlyMetAspArgSerGlySerThrAlaValAlaGlyValMetIleSerTrpYstHisIle 144
Oy 789 TATATTTGCCAACTCGAGATAGTCGGGCAATCTTGTGCTTATTAATGAGAGATCAA 848
    |||
    |||
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Db 145 TyrPheIleAsnCysGlyAspSerArgAlaValLeuTyrArgAsnGlyGln----- 161
Oy 849 AAACATGACAGCCTTAAGCCTCAGCAAAAGCATTAATCCAGTACGATGAAGCGCATG 908
    |||
    |||
Db 162 -----ValCysPheSerThrGlnAspHisIleYstProCysAsnProArgIstYstGlu 178
Oy 909 AGGATTAAGAAAGCTGAGAGAAACGTCAAGGATGGCGCTGTTTGGGCGGTGTAAGGTG 968
    |||
    |||
Db 179 ArgIleGlnAsnAlaGlyGlySerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
Oy 969 TCACGCTCCATTTGGGAGACGGGACATCAAGCGCTCCGT----- 1007
    |||
    |||
Db 199 SerArgAlaLeuGlyAspTyrAspTyrAspTyrCysValaIleAspGlyIYstProThrGluGln 218
Oy 1008 ---GTCACCTCTGTGTCGCCGACATCAAGCGTCCAGCTGACCCCAATGACAGGTTCAAT 1064
    |||
    |||
Db 219 LeuValSerProGluProGluValIYstIleLeuAlaGluGluAspGluPheIle 238
Oy 1065 TTGTTGGCCTGTGATGGCTCTTCAAGGTCTTTACCCCAAGAAAGCCGTGAATTCATC 1124
    |||
    |||
Db 239 IleLeuAlaCysAspGlyIleTrpAspValMetSerAsnGluGluLeuCysGluTyrVal 258
Oy 1125 TTGTCCTGTCGAGAGTAAAGATCCAGACCCGGAGGAGAAAGTCCGACCCGACGCC 1184
    |||
    |||
Db 259 LysSerArgLeuGlu-----ValSerAsp 266
Oy 1185 CGCTACGAAGCAGCCTCGCAACAGCGTCGCCAACAGGCGGTGACGGGGCTCGGCCGAC 1244
    |||
    |||
Db 267 AspleuGluAsnValCyAsnTrpValValAspThrCysLeuHisIleuSglYserItrAsp 286
Oy 1245 AACGTCACTGTGATGGTGGTG 1265
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Db 287 AsnMetSerIleValLeuVal 293

RESULT 20
US-09-724-676-80003
; Sequence 80003, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Comugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Comugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80003
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-80003

Alignment Scores:
Pred. No.: 5,5e-13 Length: 387
Score: 313.00 Matches: 94
Percent Similarity: 44.65% Conservative: 52
Best Local Similarity: 28.75% Mismatches: 125
Query Match: 12.23% Indels: 56
DB: Gaps: 8

US-09-935-124A-1 (1-1422) x US-09-724-676-80003 (1-387)
Oy 333 AAGAGAAAACCTCGAGAGAGAAAGATGCGACGTGAGAGACTTGTGGAAAAGAAATT 392
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    |||
Db 7 LysProlYstHnGluYstHnIleAsnAlaHisGlyAlaGlyAsn----- 20
Oy 393 TGTAAAGCCTCTTCGGTATCTTGGTGTGAAGGCGCTATGCGTCAAGCGGAAGGTGAG 452
    |||
    |||
Db 21 -----GlyLeuArgTyrGlyLeuSerSerMetGlnIYTrp 32
Oy 453 AGGAGAGATGACAGATGCCACGTCACTCTGAACGACATCAACGAGAGGTGAAGCCC 512
    |||
    |||
Db 33 ArgValAlaGluMetGluAspAlaHisIstHraIaValAlaGlyIle----- 46
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Db      44  ProAspAlaArgProValArgSerProAlaArgGlyArgThrLeuProTrpAsnAlaGly 63
Qy      330  ---GCAAGAGAGAAAACTCCGAGAGAGAGAAAGATGGAGATGGAAGCTTGGGAAAAG 386
Db      64  TyrAlaGluValIleAsnAlaGluLysSerGluPheAsnGluAspGlnAlaAlaCysGly 83
Qy      387  AAGGTTTGAAGGCTCTTGGGTATCTTTGGCTGGAAGGGGTATGGCTGAGCCGGAAG 446
Db      84  LysLeuGly---IleArgArgCysGluPheGlyIle----- 94
Qy      447  GGTGAGAGGAGAGATCCAGATGCCAGTCATCTGAAAGACATCCAGAGAGTGT 506
Db      95  -----GluGlnHisGlnGluTrpLeuThrVal-----Cys 104
Qy      507  AGGCCCCATCGCTCCCTCATTAATCTCGGGTTTCAATTGCTGTTTGGATGACATGGA 566
Db      105  ---ProGluGluPheLeuThrGly---HisTyrTrpAlaLeuPheAspGlyHisGly 121
Qy      567  GGAATTGAGCTCAAAATTTGCTGCACAGATTTGCATCAAACTTAATCAGA----- 620
Db      122  GlyProAlaAlaAlaIleLeuAlaAlaAsnThrLeuHisSerCysLeuArgArgGlnLeu 141
Qy      620  ----- 620
Db      142  GluAlaValValGluGlyMetIleAlaProGlnProPheMetHisLeuSerGlyArgCys 161
Qy      621  -----AAATTCCTAAGAGATGTAATCAAGTGTGAGAAAACCGTG 662
Db      162  ValCysProSerAspProGlnPheValGluGlyIleGlnAlaGluAspLeuVal 181
Qy      663  AAGAGATGCTTTTGGACATTTCAACAGTACTGATGAAGAGTTCCTTAA-----CAA 716
Db      182  IleGlyAlaLeuGluAsnAlaPheGlnGlnCysAspAspValIleGlyArgGluLeuGlu 201
Qy      717  GCTTCCAGCCAGAGCTGCTGGAAGATGGGTCCATGCGCAGCTGTTCTGGCTGTA 776
Db      202  AlaSerGlyGln-----ValGlyGlyCysThrAlaLeuValAlaValPheLeu 217
Qy      777  GACACATCTTTATATTGCCAACCTCGAGATAGTCGGCAATCTTGTCGTTATAT 836
Db      218  GlnGlyLysLeuTyrValAlaAsnAlaGlyAspSerArgAlaIleLeuValArg----- 235
Qy      837  GAGAGAGTCAAAACATGCAGCTTAAGCTCAGCAAGAGCATATATCAACTCAGTAT 896
Db      236  -----ArgHisGluIleArgGlnLeuSerSerGluPheThrProGlu----- 249
Qy      897  GAAGACGGATGAGATACAGAG-----GCTGGA-- 926
Db      250  ThrGluArgGlnArgIleGlnGlnLeuAlaPheThrTyrProGluLeuLeuAlaGlyGlu 269
Qy      926  ----- 926
Db      270  PheThrArgLeuGluPheProArgArgLeuLysGlyAspAspLeuGlyGlnLysValLeu 289
Qy      926  ----- 926
Db      290  PheArgAspHisHisMetArgGlyTyrSerTyrLysArgValGlnLysSerAspLeuLys 309
Qy      927  -----GGAACGTCAGGAGATGGCGTGTGGTGGCGTGTGAGAGTGTCA 971
Db      310  TyrProLeuIleHisGlyGlnGlyArgGlnAlaArgLeuLeuGlyThrLeuAlaValSer 329
Qy      972  CGCTCCATTGGGAGCGGAGTACAG-----CGCTGCGGT 1007
Db      330  ArgGlyLeuGlyAspHisGlnLeuArgValLeuAspThrAspIleGlnLeuLysProPhe 349
Qy      1008  GTCACTCTGTGCCC-----GACATCAGACGCTGCAGCTGACAGCCCAAT 1052
Db      350  LeuLeuSerIleProGlnValThrValLeuAspValHisGlnLeuAlaValGlnGlu 369
Qy      1053  GACAGGTCATTTTGGCGCTGTGATGGGCTCTTCAAGGCTCTTACCCAGAGAGAGCC 1112
Db      370  Asp---ValValValMetAlaThrAspGlyLeuTrpAspValLeuSerAsnGluGlnVal 388

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Qy      1113  GTGAATTCATCTTGCTGCTGCTGAGATGAAAAG----- 1148
Db      389  AlaLeuLeuValArgSerPheLeuThrGlyAsnGlnLysAspAspProHisArgPheSer 408
Qy      1149  -----ATCCAGACCCGGAGAGGAAAGTCCGCGAGCGGAGCGCGGTAC 1190
Db      409  GluLeuAlaLysMetLeuIleHisAsnThrGlnGlyLysAsp----- 422
Qy      1191  GAACGACCTGCACACAGCTGCGCCACACAGCGGTGACCGGCG-----TCGGCCGAC 1244
Db      423  -----AsnGlyAlaThrGlyGluGlyGlnValSerTyrAsp 434
Qy      1245  AACGTCACTGTATGTGTGTGGATAGAGCACTGAAGGGGTGGCGCGCCAGAGAC 1304
Db      435  AspValSerValPheValIleProLeu---HisSerGlnAlaGlnGluGlySerGlyHis 453

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Search completed: February 9, 2003, 18:12:01
 Job time : 60.5 secs

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/ LENGTH: 306 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM: Rattus
/
US-08-822-701-8

Alignment Scores:
Pred. No.: 1,66e-26 Length: 306
Score: 340.00 Matches: 101
Percent Similarity: 49.33% Conservative: 47
Best Local Similarity: 33.67% Mismatches: 104
Query Match: 13.28% Indels: 48
DB: Gaps: 12

US-09-935-124A-1 (1-1422) x US-08-822-701-8 (1-306)
OY 417 GCTCTGAAGGCTATGCTGCTGAGCGGAGGAGGAGGAGATGACAGATGCCAC 476
DB 21 GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTyrPArgValGluMetGluAspAlaHis 40
OY 477 GTCATCTGAACGATCACCGAGAGGTGATAGCCGCCCATGCTCCCTATTACTCGGGTT 536
DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGluThr---Trp 53
OY 537 TCATATTTTCTGTTTGTATGATGACATGAGAAATTCAGACCTCAAAATTTGCTGCACAG 596
DB 54 SerPhePheAlaValTyrAspGlyHisAlaGlySerGlnAlaAlaTyrTyrCysGlu 73
OY 597 AATTGCATCAAACTTAATCAGAAATTTCTT---AAGAAGAT---GTAATCACT 647
DB 74 HisLeuLeuAspHisIleThrAsnAsnGlnAspPheLeuGlySerAlaGlyAlaProSer 93
OY 648 GTAGAGAAACCTGTAAGAGATGCTTTTGGACATTTCAAGCATATCGATGAAGATTC 707
DB 94 ValGlu---AsnValIleAsnGlyLeuArgThrGlyLeuGluGluLeuAspGluHisMet 112
OY 708 CTTAAACAAGCTTCCAGAACGCTCTTGGACATTTCAAGCATATCGATGAAGATTC 767
DB 113 ArgValMetSerGluLeuLysHisIleGlyAlaAspArgSerGlySerThrAlaValGlyVal 132
OY 768 CTGGCTGTAGACAACATCTTTATATGCTCAACCTCGAGATGTGGGCAATCTTGCT 827
DB 133 LeuIleSerProGlnHisThrTyrPheIleAsnGlyLeuAspSerArgGlyLeuLeuGlyCys 152
OY 828 CATTATATGAGAGAGACTCAAAACATGACGCTTAAGCCTCGACAAAGAGATATATCCA 887
DB 153 Arg-----AsnArgLysValHisPhePheThrGlnAspHisIleGlyPro 166
OY 888 ACTCAATATGAAAGCCGATGAGATACAGAAAGCTGAGAGAAACCTCAAGAGATGGGCT 947
DB 167 SerAsnProLeuGluLysGluArgIleGlnAsnAlaGlyLeuSerValMetIleGlnArg 186
OY 948 GTTTTGGGCTGTAGAGGTGTACGCTTCATTGGGGAAGCGGCAATCAAGCGCTGC--- 1004
DB 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGlyAspPheAspTyrLys---CysVal 205
OY 1005 -----GGTGTACCC-----TCGTGCCCGCAATCAAGA 1031
DB 206 HisGlyLysGlyProThrArgGluGlnLeuValSerProGluProGluValHisAspIleGlu 225
OY 1032 CCGCTGCAGCTGACCCCAATGACAGATTCAATTTGTGGCTGTGATGGGCTCTTCAAG 1091
DB 226 ArgSerGlu-----GluAspAspGlnPheIleIleLeuAlaCysAspGlyIleTrpAsp 243
OY 1092 GTCCTTACCCCAAGAGAGCGGTGACATTCATCTGCTGCTCGAG-----GATGAA 1145
DB 244 ValMetGlyAsnGluGluLeuGlyAspPheValArgSerArgLeuGluValThrAspAsp 263

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OY 1146 AAGATCCAGACCCGGGAAGGGAATGCCGAGCCGACGCCCTACGAAAGAGCTTGCAAC 1205
DB 264 -----LeuGluLysValCysAsn 269
OY 1206 AGCGTGGCCACAGAGCGGTGACGCGGGGCTGCGCCGACAAAGTCACTGATGATGGTGG 1265
DB 270 GluValValAspThrCysLeuTyrLysGlySerArgAspAsnMetSerValIleLeuIle 289

RESULT 3
US-08-935-855-8
/ Sequence 8, Application US/08935855
/ Patent No. 6086485
/ GENERAL INFORMATION:
/ APPLICANT: Galun, David, Mark
/ TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
/ TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, P1N13
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: David A. Jackson, Esq.
/ STREET: 411 Hackensack Ave, Continental Plaza, 4th
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/935,855
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson, Esq. David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 306 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE:
/ ORIGINAL SOURCE:
/ ORGANISM: Rattus
/
US-08-935-855-8

Alignment Scores:
Pred. No.: 1,66e-26 Length: 306
Score: 340.00 Matches: 101
Percent Similarity: 49.33% Conservative: 47
Best Local Similarity: 33.67% Mismatches: 104
Query Match: 13.28% Indels: 48
DB: Gaps: 12

US-09-935-124A-1 (1-1422) x US-08-935-855-8 (1-306)
OY 417 GCTCTGAAGGCTATGCTGCTGAGCGGAGGAGGAGATGACAGATGCCAC 476
DB 21 GlyLeuArgTyrGlyLeuSerSerMetGlnGlyTyrPArgValGluMetGluAspAlaHis 40
OY 477 GTCATCTGAACGATCACCGAGAGGTGATAGCCGCCCATGCTCCCTATTACTCGGGTT 536
DB 41 ThrAlaValIleGlyLeu-----ProSerGlyLeuGluThr---Trp 53

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Oy 537 TCAATATTTGGCTTTTGTATGAGCAATGAGAAATTCAGACCTCAAAATTTGCTCAGC 596
Db 54 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||::: 73
Oy 597 AATTTCATCAAACTTAATTCAGAAAATTTCCCT---AAAGAGAT-----GTAATCAGT 647
Db 74 |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::||||| 93
Oy 648 GTAAGAGAAACCGTGAAGAGATGCTTTTGGACATTTCAAGCATCTGATGAAGATTC 707
Db 94 ValGlu---AenValIyAenGluIleArgThrGlyPheLeuGluIleAspGluHisMet 112
Oy 708 CTTAAACAAGCTTCAGCAGAAAGCCCTCGGAAAGATGGGTCACCTCCACGCTGTT 767
Db 113 ArgValMetSerGluIyIyVbHISglYAlAspArgSerIySerThrAlaValAlaIyAl 132
Oy 768 CTGGCTGTAGCAACATTTCTTATATATGTCACACCTCGAGATAGTGGCAATCTTGAT 827
Db 133 LeuIleSerProGlnHisIleThrIyPheIleAsnCyGclYAspSerIyGclYleuLeuCyS 152
Oy 828 CGTTATTAATGAGAGAGCTCAAAAACATGACGCTTAAGCCTCAGCAAAAGACATATCA 887
Db 153 Arg-----AenArgIyValHisPhePheThrGlnAspHisIyAspPro 166
Oy 888 ACTCAGTATGAAGAGCGGATGAGGATCACAAGAAGCTGAGAGAAACCTCAGGATGGCGT 947
Db 167 SerAsnProLeuGluIyVbGluArgIleGlnAsnAlaGlyIySerValMetIleGlnArg 186
Oy 948 GTTTTGGGCTGTGAGAGGTGCACGCTCCATTTGGGAGCGAGCATGACAAAGCGCTGC--- 1004
Db 187 ValAsnGlySerLeuAlaValSerArgAlaLeuGclYAspPheAspIyIyS---CySerAl 205
Oy 1005 -----GGTGTACC-----TTGTGCCCCGACATCAGA 10311
Db 206 HisGluIyGclYProThrGluGlnLeuValSerProGluIyProGluIyAlHisAspIleGlu 225
Oy 1032 CGCTGCCAGCTGACCCCCCATGACAGGTTATTTGTGGCTCTGTATGGCTCTTCAAG 10919
Db 226 ArgSerGlu-----GluAspAspGlnPheIleIleLeuAlaCyAspAspIyIleThrAsp 243
Oy 1092 GTCTTTATCCCGAAGAAGACCGGTGAATCTCATCTTGTCTGTCTGACG-----GATGA 11455
Db 244 ValMetGlyAsnGluIyGluLeuCyAspPheValArgSerArgLeuGluIyAlaThrAspAsp 263
Oy 1146 AAGATCCAGACCCGAGAAAGGAAAGTCCGACGCCGACCCGCTACGAAACAGCCTGCAAC 1205
Db 264 -----LengIuIyValCyAsn 269
Oy 1206 AGCGTCGCAACAGAGCGGTGCACCGGGCTCGGCGCGACAGCATCTCATGTAGTGGTG 12655
Db 270 GluValIyAlaSerThrCyLeuIyIyGclYSerArgAspAspMetSerValIleLeuIle 289

RESULT 4
US-09-206-646-4
: Sequence 4, Application US/09206646
: Patent No. 6436637
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Goli, Surya K.
: APPLICANT: Lal, Preeti G.
: APPLICANT: Cortley, Neil C.
: APPLICANT: Zhang, Hong
: TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
: FILE REFERENCE: PF-0319-1 DIV
: CURRENT APPLICATION NUMBER: US/09/206,646
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PERL Program
: SEQ ID NO 4
: LENGTH: 390
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:

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NAME/KEY	misc feature	ID No.	6436637	g452526
OTHER INFORMATION: ID No. 6436637 g452526				
US-09-206-646-4				
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Pred. No.:	5,36e-25	Length:	390	
Score:	326.00	Matches:	98	
Percent Similarity:	45.87%	Conservative:	52	
Best Local Similarity:	29.97%	Mismatches:	121	
Query Match:	12.73%	Indels:	56	
DB:	4	Gaps:	10	
US-09-935-124A-1 (1-1422) x US-09-206-646-4 (1-390)				
QY	333	AAGAGAAAACTCCGAGAGAGAGAAAGAAATGGCAGTGAAGAGCTTGAGAAAAAGT	392	
DB	7	LYSPROLYSTRGILUYSHLSAENALAHLSGLYLAAGLYAEN-----	20	
QY	393	TGTAAAGCTCTTGCGTGATCTTTGGTCTGCAAGGCGTANGTGGCTGACGGAAAGGTGAG	452	
DB	21	-----GlyLeuAlaGlyGlyLeuSerSerMetClnLYTP	32	
QY	453	AGGGAGAGATGCAGATGCGCCAGCATCCATCCAAAGCATACCGAGAGAGTATGCGCC	512	
DB	33	ArgValAlaGluMetGluAraAlaHisThrAlaValAlaGlyLeu-----	46	
QY	513	CCATGTCCTCATTTACTCGAGGTTCATATATTTGCTGTTTGTATGACATGAGGAAT	572	
DB	47	ProHISgLYeu---AraPantTrpSerPhePheAlaValItyrAspGlyHISlaGlySer	65	
QY	573	CGAGCTCCAAAATTGCTGCAKAGAAATTGCATCAAACTTA-----ATC	617	
DB	66	ArgValAlaAsnTYrCySerSerThrHISLeuLeuGluHISLeThrThrAsnGluAraPhe	85	
QY	618	AGAAAATTCTCTAAA---GGAGATGTATATC-----AGTGTAGAGAAAACGTGAAGAGA	668	
DB	86	ArgAlaAlaAspIyrsSerGlySerAlaLeuGluProSerValGlu---SerValIystr	104	
QY	669	TGCTTTTGGACATTTTCAAGCATACTAGTGAAGATTCCTTAAACAAGCTTCGAGCAG	728	
DB	105	GlyIleAthrThrglyPheLeuIySileAspGluTYrMetArgAsnPheSerAspLeuArg	124	
QY	729	AAGCTGCTGGAAGAAGTGGGTCCACTGCCAGCTGTGTTCTGCGCTGTAGACAACATTTT	788	
DB	125	AsnGlyMetAspArgSerGlySerThrAlaValAlaGlyValMetValSerProThrHisMet	144	
QY	789	TATATTCGCAACCTCCGAGATAGTACGGGCAACTTGTCGCTTAATAGAGAGAGTCA	848	
DB	145	TYrPheIleAsnCySgIyAspSerAspAlaValAlaLeuCyAraAsnGlyGln-----	161	
QY	849	AAACATGACAGCTTAAAGCTCCACAAGAGACATATCCAACTCAGTATGAAGAGCGCATG	908	
DB	162	-----ValCyPheSerThrGlnAraPheHISlyPProCyAsnProValGluIySle	178	
QY	909	AGCATACAGAAAGCTGAGAGAAAGCTCAGGAGTGGCGTGTGTTGGCGCTGTAGAGTG	968	
DB	179	ArgIleGlnAsnAlaGlyIySerValMetIleGlnArgValAsnGlySerLeuAlaVal	198	
QY	969	TCAGGCTCCCAATGGGAGCGGAGAGTTCACAGCGCTGGCGT-----	1007	
DB	199	SerArgIleAsnGlyAspTYrAspTYrLysCyValAspGlyIySgIyProThrGluGln	218	
QY	1008	---GTCACTCTGTGCGCCGACATCAACCGCTCCAGCTGACCCCAATGACAGGTTTCAT	1064	
DB	219	LeuValSerProGluProGluValItyrGluIleValAlaGluAlaGluIyAspGluPheVal	238	
QY	1065	TTGTGGCTGTGTATGGGCTCTTCAAGGCTTTTACCCAGAGAAAGCGGTAACTTATC	1124	
DB	239	ValLeuAlaCysAspGlyIyIetTrpAspValMetSerAsnGluGluIyLeuCyGluPheVal	258	
QY	1125	TTTGCTCTGTCTCGAGATGAAGAAATCCAGACCCGAGAAAGGAATCCGACAGCGACCC	1184	
DB	259	LYSPSTRGILUENGU-----ValSerAsp	266	


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OY 1185 CCCTACGAAGCAGCTCCCAACAGCTGCGCAACAGCGGCTGCGCCGAC 1244
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 267 AsplegulinanValCysAsnTrpValAspThrCysLeuHISLysGlySerArgAsp 286
OY 1245 AACGTCACTGATGATGATG 1265
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Db 287 AsnMetSerValValLeuVal 293

RESULT 5
US-08-822-701-7
/ Sequence 7, Application US/08822701
/ Patent No. 5976853
/ GENERAL INFORMATION:
/ APPLICANT: Guthridge, Mark
/ APPLICANT: Basilio, Claudio
/ TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
/ TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSES: David A. Jackson, Esq.
/ STREET: 411 Hackensack Ave, Continental Plaza, 4th
/ STREET: Floor
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/822,701
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq. David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 1049-1-002 N
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 309 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
/ FRAGMENT TYPE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Mus musculus
/ US-08-822-701-7

Alignment Scores:
Pred. No.: 1,72e-24 Length: 309
Score: 320.50 Matches: 98
Percent Similarity: 46.06% Conservative: 54
Best Local Similarity: 29.70% Mismatches: 115
Query Match: 12.52% Indels: 63
DB: 2 Gaps: 12

US-09-935-124A-1 (1-1422) x US-08-822-701-7 (1-309)
OY 333 AAGAGAAAGCTCCGAGAAAGAAAGATGCGATGAAGCTTGGAAGAAAGTT 392
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Db 7 LysProlYshHglYshSAsnAlaHISglYAlaGlyAsn----- 20
OY 393 TGTAAAGCTCTTGGTGAATCTTTGGTCTGAAGGCTATGAGCTGAGCGGAAGGTGAG 452
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 -----GlyLeuArgTyrTglYLeuSerMetCIndYTrp 32

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OY 453 AGGAGAGATGACAGATGCCCACTGATCTTGAAACGATCAACCGAGAGTAAAGCCC 512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 33 ArgValGluMetGluAspAlaHISThrAlaValGlyLe----- 46
OY 513 CCATGTCCTTCATTAATCTCCGATTTGATATTTGGTGTGTTGATGACATGAGGAATT 572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 ProHISGlyLeu--AspAsnTrpSerPhePheAlaValYAspPoliHISAlaGlySer 65
OY 573 CGAGCTCAAAATTGCTGCAAGAAATTGTCATCAAAACTTA-----ATC 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 66 ArgValAlaAspYsSerThrHISLeuGluHISThrThrAsnGluAspPhe 85
OY 618 AGAAATTTCTTAA--GGAGATGTAATC-----AGTGAAG-----AAACCTGG 662
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 ArgAlaAlaAspYsSerGlySerAlaLeuGluProSerValGlySerValYshHglY 105
OY 663 AAGAGATGCTTTTGACACTTTCAGACACTGATGTAAGAGTTCTTAAACAGCTTCC 722
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 106 ArgThrGlyPheLeuYsLe-----AspGluYrMetArgAsnPheSer 120
OY 723 AGCCAGAACCTGCTGG--AAAGATGGATCCACTGCGACAGTGTGCTGCTGAGAC 779
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 AspleuArgAsnGlyMetAspArgSerGlySerThrAlaValGlyValMetValSerPro 140
OY 780 AACATCTTTATATGCGCAACCTCGAGATAGTGGGCAATCTGTGCTTAAATGAG 839
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 141 ThHISMetTyrPheHISAsnYsGlyAspSerArgAlaValLeuYsArgAsnGlyGln 160
OY 840 GAGAGTCAAAACATGCAAGCTTAAAGCTTCAAGAAAGCATTAATCCAACTCAGTATGAA 899
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 -----ValCysPheSerThrGlnAspHISLysProCysAsnProVal 174
OY 900 GAGCGATAGATATACAGAAAGCTGAGAGAAAGCTGAGGAATGGCCGCTTTGGCGGTG 959
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 175 GluYshGluArgLISglHISAsnAlaGlyLysValMetCIndGlnYsValAsnGlySer 194
OY 960 CTAGAGTGTCAAGCTTCATTTGGGAGCGGCACTACAAAGCTGCGGT----- 1007
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 195 LeuAlaValSerArgAlaLeuGlyAspTyrAspTyrLysCysValAspGlyYsGlyPro 214
OY 1008 -----GTACCTCTGTGCTCCGAGACATGACAGCGTGCAGCTGACCCCAATGAC 1055
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 215 ThrGluGlnLeuValSerProGluProlGluValYrGluHISValArgAlaGluGluAsp 234
OY 1056 AGTTTCATTTTGTGAGCTGTGATAGGCTCTTCAGGCTTTTACCCAGAAAGCCGTG 1115
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 235 GluPheValValLeuHISLysAspGlyLISLysValMetSerAsnGluGluLeuCys 254
OY 1116 AACTTCATCTTCTGCTGCTGAGAGTGAAGATCCAGACCCGGGAGAGAGTCCGCA 1175
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 GluPheValYsSerArgLeuGlu----- 262
OY 1176 GCCAGAGCCCGCTACAGAACGCTGCAACAGCGTGGCCAAACAGCGGATGACGGAGC 1235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 263 ValSerAspAspLeuGluAsnValCysAsnTrpValValAspThrCysLeuHISLysGly 282
OY 1236 TCGGCCACACAGCTCACTGTATGATGATG 1265
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 283 SerArgAspAsnMetSerValValLeuVal 292

RESULT 6
US-08-935-855-7
/ Sequence 7, Application US/08935855
/ Patent No. 6066485
/ GENERAL INFORMATION:
/ APPLICANT: Guthridge, Mark
/ APPLICANT: Basilio, Claudio
/ TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
/ TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSES: David A. Jackson, Esq.

```



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Db 66 ArgValAlaIaenTyrCySerThrHisLeuLeuGlnHisIleThrThraBngIuaPhe 85
Qy 618 AGAAATTTCTTAAGAGAGATGTAATC-----AGTGTAGAGAAAACCGTAGAGA 668
Db 86 ArgAlaAlaIaerYsSerGlyPheAlaLeuGlnProSerValGlu---AsnValIysThr 104
Qy 669 TGCCTTTTGGACATTTCAAGCACTACTGATGAAGAATTCTTTAAACAGTTCCAGCCG 728
Db 105 GlyIleArgThrGlyPheLeuYsIleAspGluTyrMetArgAsnPheSerLeuArg 124
Qy 729 AGCCGCGCTGGAAGAATGAGATGCGACAGCTGCTTGGCTGTAGACAACTTTCTT 788
Db 125 AsnGlyMetAspArgSerGlySerThrAlaValGlyValMetIleSerProthriIle 144
Qy 789 TATATGCGAACTTCGAGATAGTCCGGCAATCTTGTCGTATATAGAGAGAGTCAA 848
Db 145 TyrPheIleAsnCySerGlyAspSerAlaValLeuCyAsnArgAsnIyGln----- 161
Qy 849 AAACATGACGCTTAAGCTTACGCAAAAGACATATCCAACTGATATGAAGCGGATG 908
Db 162 -----ValCyAspSerThrGlnAspHisIleYsProCyAsnProMetGluYsGlu 178
Qy 909 AGGATACAGAGCTGAGAGAAACGTCAGGAGATGGCGCTTTGGCGCTTACAGGTG 968
Db 179 ArgIleGlnAsnAlaGlyIysSerValMetIleGlnArgValAsnGlySerLeuAlaVal 198
Qy 969 TCAGCTCCATTGGGAGCGGAGTACAAAGCGCTGCGGT-----1007
Db 199 SerArgAlaLeuGlnIyAspTyrIyAspTyrIySAspValAspIyYsGlyProthriGln 218
Qy 1008 ---GTCACTCTGTGCCCCGACATCAAGCGCTGCACCTGACCCCAATGACAGTTTCA 1064
Db 219 LeuValSerProGluProGluValTyrGluIleLeuArgAlaGluIuAspGluPheVal 238
Qy 1065 TTGTTGGCTGTGATGGGCTCTTCAAGTCTTTAACCCAGAAAGACCGGAACTTCATC 1124
Db 239 ValLeuAlaCyAspIyIleIleTyrAspValMetSerAsnGluIuLeuCyGluIuPheVal 258
Qy 1125 TTGTCTGTCTCGAGATGAAAGATCCAGACCCGGAAAGGAAGTCCGACCGCAGCC 1184
Db 259 AsnSerArgLeuGlu-----ValSerAsp 266
Qy 1185 CCGTACGAAGACGCTGCAACAGGCTGGCCACAGGCGGTGACCGGCTTCGCGCAG 1244
Db 267 AspLeuGlnAsnValCyAsnThrValIAspThrCyLeuHisIySAspSerArgAsp 286
Qy 1245 AACGTCACTGTATGTGTGTG 1265
Db 287 AsnMetSerIleValLeuVal 293

RESULT 9
US-08-822-701-9
; Sequence 9, Application US/08822701
; Patent No. 597853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSER: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1664
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
;
US-08-822-701-9

Alignment Scores:
Pred. No.: 3,32e-24 Length: 281
Score: 317.50 Matches: 95
Percent Similarity: 45.87% Conservative: 44
Best Local Similarity: 31.35% Mismatches: 93
Query Match: 12.40% Indels: 71
DB: 2 Gaps: 12

US-09-935-124a-1 (1-1422) x US-08-822-701-9 (1-281)

Qy 432 GTGGCTGAGCGGAAGGTGAG-----AGGAGAGATGACAGATCCCACTCATCTG 485
Db 23 ValAlaGlnAsnIleGlyAsnSerIyAspPheArgTyrHisIleThrTyrVal 42
Qy 486 AACGACATCACCGAGAGAGTGAAGCCCATGCTCCATTACTCGGGT-----TCA 539
Db 43 LysAsnPheAla-----SerArgLeuAspTrpGly 52
Qy 540 TATTTTGTCTGTTTGTATGACATGAGAGAAATTCAGCCTCAAAATTTGCTGCACAGAT 599
Db 53 TyrPheAlaValPheAspIyHisIleGlyIleGlnIleAspTyrCysGlyYsHis 72
Qy 600 TTGCAT-----CAAACTTAATCAGAAAATTTCTTAAGAGATTAATCACT 647
Db 73 LeuHisThrIleIleGluGlnAsnIleLeu-----AlaAsp 84
Qy 648 GTAGAGAAACGCTGAGAGATGCTTTTGGACATTTCAAGCATACTGATGAAGTTC 707
Db 85 GluThrArgAspValArgAspValLeuAsnAspSerPheLeuAlaIleAspIuGluIle 104
Qy 708 CTTAAACAAGCTTCAGACGAGAGCTGCTGGAAGAATGGTTCACCT---GCCAGTGT 764
Db 105 -----AsnThrIySAspValGlyAsnSerGlyCyThrAlaIaIaValCys 119
Qy 765 GTTCTG-----GCTGTAGACAACAT-----785
Db 120 ValLeuArgTyrGluLeuProAspSerValSerAspSerMetAspLeuAlaGlnHis 139
Qy 786 -----CTTATATGCGCAACCTCGAGATAGTCCGGCAATCTGTGTGTTATAT 836
Db 140 GlnArgIySLeuTyrThrAlaAsnValGlyAspSerArgIleValLeuPheArgAsnGly 159
Qy 837 GAGAGAGTCAAAAACATGACGCTTAAGCCTCAGCAAAAGCATATCACTGAGTAT 896
Db 160 Asn-----SerIleArgLeuThrTyrAspHisIySAspSerArg 173
Qy 897 GAAGAGCGGATGAGATACAGAAAGCTGAGAGAAACGTCAGGAGATGGCGCTTTGGGC 956
Db 174 LeuGluMetGlnArgValGlnGlnIaGlyIyLeuIleMetIySerArgValAsnGly 193

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Db	120	ValHisIleuGlnValGlyAsnValGlyAspSerThrValValAlaCys-----	135
Qy	840	GAGAGTCAAAAACATGACGCTTAAAGCTTCAGCAAAAGACATAACCTACGTATGAA	899
Db	136	-----IleAspGlyValCysValProLeuThrGluAspHisIleuSerProAsnAsnGluGly	153
Qy	900	GAGCGGATGAGGATPACAAAGAGCTGAGGAAACGTACAGGATGGCGCTGTTGGCGCTG	959
Db	154	GluArgGlnArgIleGluAsnCysValArgIleValGluAsnAsnArgValAspGlySer	173
Qy	960	CTAAGAGTGTACGCTCCATGGGAGCGGGCAGTACAG-----	998
Db	174	LeuAlaValSerArgAlaPheGlyAspArgGlnTyrIleuGlySerGlySerGlnLeu	193
Qy	999	CGCTGGGTGTACCTCTGTGCTGCGACATCAGACGCTCCAGCTGACC-----CCCAAT	1052
Db	194	GluGlnIleValIleAlaLeuAlaAspValGlnHisIleuAspPheThrPheAspSerAsn	213
Qy	1053	GACAGGTTCATTTGTTGGCTGTGATGGGCTCTTCAAG--GTCCTTACCCAGAGAA	1109
Db	214	Asp---PheValIleuLeuCysCysAspGlyValPheGluGlyAsnPheProAsnGluGln	232
Qy	1110	GCGGTAACTTATCTTCTGCTCGAGAGATGAAAAGATCCAGACCCGGAGGGAG	1169
Db	233	ValValAlaIleValIleValGlnIleuGln-----	242
Qy	1170	TCCGACGCGACGCGCCGTACAGACGCTCGAC-----AGG	1208
Db	243	-----ThrCysAsnAspLeuAlaGluValAlaGlyArg	253
Qy	1209	CTGCGCCAAAGCGGCTGACGCGGGCTGCGCCGACACGTACCTGATGATGGTGGCGG	1268
Db	254	ValCysGluGluAlaIleGluArgIleArgAspAsnIleSerCysMetIleValGln	273
<p>RESULT 15 US-08-935-855-10 Sequence 10, Application US/08935855 Patent No. 6066485</p> <p>GENERAL INFORMATION: APPLICANT: Guthridge, Mark APPLICANT: Basilio, Claudio TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13 NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSEE: David A. Jackson, Esq. STREET: 411 Hackensack Ave, Continental Plaza, 4th STREET: Floor CITY: Hackensack STATE: New Jersey COUNTRY: USA ZIP: 07601</p> <p>COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk OPERATING SYSTEM: IBM PC compatible SOFTWARE: Patent Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/935,855 FILING DATE: CLASSIFICATION: 435</p> <p>ATTORNEY/AGENT INFORMATION: NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 1049-1-002 CIP TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800 TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 314 amino acids TYPE: amino acid STRANDEDNESS: single</p>			

QY 1209 CTGGCCACAGCGGTGCGCGGGCTCGGCCGACACCTGATGATGTGCGG 1268
DB 254 ValcylglutunilalegluargylserargaspamleiserCysmetileValGln 273

RESULT 16
US-08-822-701-2
Sequence 2, Application US/08822701
Patent No. 5976853
GENERAL INFORMATION:
APPLICANT: Guichridge, Mark
TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,701
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
US-08-822-701-2

Alignment Scores:
Pred. No.: 3,276-19 Length: 392
Score: 270.00 Matches: 109
Percent Similarity: 42.09% Conservative: 64
Best Local Similarity: 26.52% Mismatches: 147
Query Match: 10,554 Indels: 91
DB: 2 Gaps: 18

US-09-935-124a-1 (1-1422) x US-08-822-701-2 (1-392)

QY 77 CTGCGCGCTTCACCCAGCTCCGCGCATGACCTCTTCGGGAGCTTCGCGGACCGGAGCCGAGCG 136
DB 17 ValProPro-HisThrIysSerGlyIleGlyThr---GlyAspGluProGlyProGln--- 34

QY 137 CTGCGCGCGCGCGCGCGGGAAGAAGCTCGAAGAAGACCCCTGCTCTTTGATGATCTCC 196
DB 35 -----GlyLeuAsnGlyGluAlaGlyPro-----GluAsp--- 44

QY 197 CCCTCGGCGCAGAGTACTGACTCAGAGATCAGGGGAGCTTTCCTTTTGATGATCTCC 256
DB 45 ----ProSerArgGluThrProSerGlnGluAsnGlyProThrAlaLysGlyHisThrGln 63

QY 257 ACCCGCTACAGTGGCGATTCAAGTTCTCTTGCACATCATATCCAGATGTAAAGAC 316

DB 63 yheSerSerAsnSerGluHisGlyThrGluAlaGlyGlnIleSerGluProGlyThrAl 83
QY 317 TGAAGGAAAGAGAGCAAGAAAGAAAACCTCCGAGGAGAGAAATGCGATGAAGACT 376
DB 83 aThrGlyGluAlaGlyProSerCysSerSerAlaSerAspLys----- 97

QY 377 TGTGAAAAGAAAGTTGTAAAGCTCTTCGTGATCTTTGTCTGAAGGCTATGTGCG 436
DB 98 ----LeuProArgValAlaLysSerLys-----PhePheGln 108

QY 437 TGAAGCGAAGGTGAGAGGAGAGATGAGATGCCACGTCATCTCGAAGCATC 496
DB 108 uAspSerGluAspGluSerAspGluValGluGlu-----GluAspAspSe 124

QY 497 CGAGAGGTAGAGCCCGCATCGCTCCCTCATTACTGGGGTTTCATATTTGCTGTTTGA 556
DB 124 rGluGluCysSerGluAspGlu-----As 132

QY 557 TGAACATGAGAGAAATTCAGAGCTCAAAATTTGCTGACAGAAATTCAGAACTTAAT 616
DB 132 pGlyTyr-----SerSerGluGluAlaGluAsn----- 141

QY 617 CAGAAATTTCTTAAGAGATGTATCATGCTAGAGAAACCGTGAAGATGCTTTT 676
DB 142 ----GluGluAspGluAspAspThrGluGluAlaGlu----- 152

QY 677 GGACACTTCAGACATCATGATGAAGATGCTT-----AAACAAGCTTCAGCCAGAA 730
DB 153 -----GluAspAspAspGluGluMetValProGlyMetGluGlyLysGluGlu 169

QY 731 GCGTGCCTGGAAGATGGGTCCACTGCCAGCGTGTCTGCTGTAGACAACTCTTTA 790
DB 169 uProGlySerAspSerGlyThrThrAlaValAlaLeuIleArgLysGlnLeuIle 189

QY 791 TATTGCCAAGCTCGAGATAGTCGGCAATCTTGTCGTGTTAATGAGAGATCAAA 850
DB 189 eValAlaAsnAlaGlyAspSerArgCysValVal-----SerGluAla 203

QY 851 ACATGACGCTTAACCTCAGCAAGCAAGATTAATCACTCATGTAAGAGCGGATGAG 910
DB 203 aGlyLysAlaLeuAspMetSerTyrAspHisLysProGluAspGluValGluLeuAlaTr 223

QY 911 GATACAGAAGCTGAGAGGAACGTC---AGGATGAGGCGTGTGTCGCTGACAGGT 967
DB 223 gLleLysAsnAlaGlyGlyLysValThrMetAspGlyArgValAsnGlyGlyLeuAsnLe 243

QY 968 GTACGCTTCATTGGGAGACGGGACGATCAAGCGTGGCT----- 1007
DB 243 uSerArgAlaIleGlyAspHisLysPheTyrLysArgAsnLysAsnLeuProProGlnGluGln 263

QY 1008 ----GTACGCTGTGCGCGCATCATCAGACGCTGCCAGACCCCAAGACAGGTTTCA 1063
DB 263 mMetIleSerAlaLeuProAspPheLysValLeuThrLeuThrAspAspHisGluPhe 283

QY 1064 TTTGTGCGCTGTGATGGGCTCTTCAGGCTTTTACCCAGAAAGCGGTGAACCTTCA 1123
DB 283 tValIleAlaCysAspGlyIleTrpAsnValMetSerSerGlnGluValValAspPhe 303

QY 1124 CTGTGCTGTCTC-----GAGATGAAGAAGTCCAGACCCGGGAGGGAAGTCCGACAG 1177
DB 303 eGlnSerLysIleSerGlnArgAspGluAsnGlyGluLeuArgLeuLeuSerSerIleVal 323

QY 1178 CGAGCCCGCTACAGAGACGCTGCAACAGGCTGGCCCAAGAGCGGTGACCGGGGCTC 1237
DB 323 LGIU-----GluLeuLeuAspGlnCysLeuAlaProAspThrSerGlyAspGlyTh 340

QY 1238 G---GCCGCAACGTCACTGTGATGTGATG 1265
DB 340 rGlyCysAspAsnMetThrCysIleIleIle 350

RESULT 17
US-08-935-855-2


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/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David A. Jackson, Esq.
/ STREET: 411 Hackensack Ave, Continental Plaza, 4th
/ CITY: Hackensack
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 07601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/935,855
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jackson Esq., David A.
/ REGISTRATION NUMBER: 26,742
/ REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 201-487-5800
/ TELEFAX: 201-343-1684
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 542 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Mus musculus
/
US-09-935-855-22

Alignment Scores:
Pred. No.: 3,98e-19 Length: 542
Score: 270.00 Matches: 109
Percent Similarity: 42.09% Conservative: 64
Best Local Similarity: 26.52% Mismatches: 147
Query Match: 10.55% Indels: 91
DB: 3 Gaps: 18

US-09-935-124A-1 (1-1422) x US-08-935-855-22 (1-542)
QY 77 CTCGCCCTCCACCCAGCTCCGCCATGACCTCTTCGGGGAGCTGCCGAGCCCGAGCG 136
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 167 ValProPro-HisThrLysSerGlyIleGlyThr---GlyAspGluProGlyProGln-- 184
QY 137 CTCGCCGCCGCCGGCTGCCGGAAGAAAGCTCAAGAAAGACCCCTGCTCTTGATGACCT 196
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 -----GlyLeuGlnGlyGluIleGlyPro-----GluAsp-- 194
QY 197 CCTCCGCCGAGAGTACTGACTCAGAGATCAGGGAGACCTTTCCTTTTGATGATCTCC 256
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 195 ----ProSerArgGluThrProSerGlnGluAsnGlyProThrAlaLysIleHisThrG 213
QY 257 ACCCGCTAGCAGTGGGAGTTCAGGTTCTTCCCAATCATATCCAGATGGTAAAGAC 316
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 213 yPheSerSerAsnSerGluHisGlyThrGluIleGlyGlnIleSerGluProGlyThrAl 233
QY 317 TGAAGGAAAGAGCAAGAAAGAAACCTCCGAGAAAGAGAAAGATGGCAAGAGCT 376
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 233 aThrGlyGluAlaGlyProSerCysSerSerAlaSerAspLys----- 247
QY 377 TGTGAAAGAAAGATTGTAAAGCTCTTTCGGTATCTTTGCTGAAGGCTATGTGGC 436
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 248 ----LeuProArgValAlaLysSerLys-----PhePheG 258
QY 437 TGAAGCAAGAGGTGAAGAGAGAGATGACGATGCCACGTCATCTCTGAACATCAC 496
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Db 258 uAspSerGluAspGluSerAspGluValGluGlu-----GluAspAspSe 274
QY 497 CGAGAGTGTAGGCCCCCATCGCTCCCTCATTTACTGGGTTTATATTTTGTGTTTGA 556
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 274 rGluGluCysSerGluAspGlu-----As 282
QY 557 TGAACATGAGAGAAATTCCAGCTCAAAATTGCTGCACAGAAATTGCATCAAACTTAAT 616
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 282 pGlyTyr-----SerSerGluGluIleGluAsn----- 291
QY 617 CAGAAATTCTCTAAAGAGATGTAATCAGTGTAGAGAAACCGTGAAGATGCTTTT 676
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 ----GluGluAspGluAspAspThrGluGluIleGlu----- 302
QY 677 GGACACTTTCACAGCATATCATGATGAAGATTCCTT-----AAACAAGCTTCCAGCAGAA 730
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 -----GluAspAspAspGluGluIleGluIleValAlaLeuIleArgGlyLeuGlu 319
QY 731 GCCTGCTGGAAGAAAGATGGGTCCATGCCACGTGTCTTGGCTGTAGACAACATTTCTTA 790
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 319 uProGlySerAspSerGlyThrThrAlaValAlaLeuIleArgGlyLeuGlu 339
QY 791 TATTGCCAACTCCGAGATGATCGGGCAATCTTGTCGCTTATATAGAGAGATCAAA 850
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 339 eValAlaAsnAlaGlyAspSerArgCysValVal-----SerGluAl 353
QY 851 ACATGAGCCTTAAGCTCAGCAAGAGCATATCAACTCATGTATGAGAGCGGATGAG 910
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 353 aGlyLysAlaAlaLeuAspMetSerTyrAspHisLysProGluuAspGluValGluLeuAla 373
QY 911 GATPACAGAAAGCTGAGAGAAAGCTC--AGGATGAGCGGTGTTTGGCGCTGATAGAGT 967
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 373 gLleLysAsnAlaGlyGlyLysValThrMetAspGlyArgValAsnGlyLeuAsnLe 393
QY 968 GTCAGCCTTCATTTGGGAGCGGCACTACAGCGCTGCGGT----- 1007
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 393 uSerArgAlaIleGlyAspHisPheTyrLysArgAsnLysAsnLeuProProGluGlu 413
QY 1008 ----GTACACTCTGTGCGCAGATCAGACGTGCGCAGCTGACCCCAATGACAGATTCT 1063
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 413 mMetLysSerAlaLeuProAspIleLysValLeuThrLysAspHisGluProPhe 433
QY 1064 TTTGTGGCTGTGATGGGCTCTTCAAGGCTTTTACCCCAAGAAAGCGTGAACCTTCAT 1123
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 433 tValIleLacCysAspGlyLysIleTyrAsnValMetSerSerGlnGluValIleAspPhe 453
QY 1124 CTTCGCTCTCTC-----GAGGATGAAAGATCCAGACCCGGGAAGGGAAGTCCGCGAC 1177
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 453 eGlnSerLysLysSerGlnArgAspGluAsnGlyGluLeuArgLeuLeuSerSerIleVal 473
QY 1178 CGAGCGCCGCTACGAGAGCGCTGCAACAGCGTGGCCAAAGAGCGGTCACGCGGCTC 1237
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 473 lGlu-----GluLeuLeuAspGlnCysLeuAlaProAspThrSerGlyAspGlyTh 490
QY 1238 G---GCCGACAAAGTCACTGTGATGGTGG 1265
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 490 rGlyCysAspAsnMetThrCysIleIleIle 500

RESULT 19
/ Sequence 20, Application US/08935855
/ Patent No. 6066485
/ GENERAL INFORMATION:
/ APPLICANT: Guthridge, Mark
/ TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
/ NUMBER OF INVENTION: SERINE/THREONINE PHOSPHATASE, FN13
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David A. Jackson, Esq.
/ STREET: 411 Hackensack Ave, Continental Plaza, 4th
/ CITY: Hackensack

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 504 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-406-854-2

Alignment Scores:
Pred. No.: 1,21e-09      Length: 504
Score: 178.00           Matches: 83
Percent Similarity: 40.88%  Conservative: 65
Best Local Similarity: 22.93%  Mismatches: 116
Query Match: 6.95%       Indels: 98
DB: 4                   Gaps: 18

US-09-935-124A-1 (1-1422) x US-09-406-854-2 (1-504)

QY 330 GCAAGAGAAAAAC-----TCCGAGAGAGAGAGATGCGATGAGAGCTTGTG 380
D 3 AlaGlnArgArgSerLeuGlnSerGlnGlnProSerTrpThrAspLeu--- 21
QY 381 GAAAAAGAAAGTTGTAAAGCCTTCCGGTG---ATCTTGTGTGAAGGGCTATGGCT 437
D 22 -----ProLeuCyHisLeuSerGlyValGlySerAlaSerAsnArgSerTyrSerAla 39
QY 438 GAGCGAAAGGAGTGAAGAGGAGAGATGCGATGCCACGTCATCCTGAACGACATCAC 497
D 40 AspGlyLysGly-----Thr 44
QY 498 GAGAGGTGAGGCCCCCATCGCTCCATTT-----ACTCGGGTTTCATAT 542
D 45 GluSerHisProProGlnAspSerTrpLeuLysPheArgSerGlnAsnLysCysPheLeu 64
QY 543 TTTCGTGTTTGTGAGCATGAGAGAAATTCGAGCCTCAAAATTTGCTGCACAGAAATTTG 602
D 65 TyrGlyValPheAsnGlyTyrArgSerGlnAsnArgValThrAsnPheValAlaGlnLysLeu 84
QY 603 CATCAAACTTAATCAGAAATTTCTTAAGGAGATGTAATCAGTGAAGAGAAACCGTG 662
D 85 SerAlaGlnLeuLeu-----LeuGlyGlnLeuAsnAlaGlnHisAlaGlnLysLeuVal 102
QY 663 AAGAGATGCTTTTGACACATTTCAAGCATCTAGTAAAGATTCCTT----- 710
D 103 ArgArgValLeuLeuGlnAlaPheAsnValValGluArgSerPheLeuGlnSerLeuAsp 122
QY 711 -----AAACAGCTTCAGCCAGAG----- 731
D 123 AsnAlaLeuAlaGlnLysPheLeuGlnSerGlnLeuProGlnGlyValProGlnHis 142
QY 732 -----CCTGCCTGAGAA----- 743
D 143 GlnLeuProProGlnTyrGlnLysIleLeuGlnArgLeuLysThrLeuGlnLysGlnLeu 162
QY 744 ---GATGGGTCCATGCGCCACGTGTCTTCTGCGCTGAGACACATTTTATATTCGCAAC 800
D 163 SerGlyGlyAlaMetAlaValAlaValLeuLeuAsnLysLeuLysValAlaAsn 182
QY 801 CTCGGAGATAGTCGGGCAATCTTGTCGTTATATGAGAGAGTCAAAAACATCAGCC 860
D 183 ValGlyThrAsnArgValLeuLeuCyHisSerThrValAspGlyLeuGln-----Val 200
QY 861 TTAAGCCTCAGCAAGACATATCAATCACTAGTATGAAGAGCGATGAGATCAGAAAG 920
D 201 ThrGlnLeuAsnValAspHisThrThrGlnAsnGlnLysArgGlnLysPheArgLeuSerGln 220
QY 921 GCTGGA-----GAAACGTCAGGAGATGGCGCTGTTTGGCGCTGAGAGGTGCA 971
D 221 LeuGlyLeuAsnArgAlaGlyLysIleLeuGlnValGlyIleLeuCyGlyGlnLysThr 240
QY 972 CGCTCCATTTGGGAGAGGCGACATCAAG---CGCTCGGTGTCACTCTGTG----- 1019
D 241 ArgArgIleGlyAsp-----TyrLysValLysTyrGlyTyrThrAspIleAsnLeuLeu 258

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QY 1020 -----CCGACATCAGACGCTGCCAGCTGACC 1046
D 259 SerAlaAlaLysSerLysProIleLeuAlaGlnProGlnLysGlyAlaGln----- 276
QY 1047 CCCCATGAC-----AGGTTCATTTTGTGGCCTGTGATGGCTTTCAAGCTCTTT 1097
D 277 ProLeuAspGlyValThrGlyPheLeuValLeuMetSerGlnGlyLeuTyrLysAlaLeu 296
QY 1098 ACC-----CCAGAGAAAGCCGTGAACCTTCATCTTGTCTGTCGAGAGATGAA 1145
D 297 GlnAlaAlaHisGlyProGlnGlnAlaAsnGlnGlnIleAlaAlaMetIleAsnPheThrGln 316
QY 1146 AAGATCCAGACCCGGGAGAGGAGATCCGACCGACCGCCGCTACAGACGCTGCAAC 1205
D 317 PheAlaLys-----GlnThrSerLeuAspAlaValAlaGlnAlaValValAsp 332
QY 1206 AGGCTG 1211
D 333 ArgVal 334

RESULT 23
US-09-529-279-2
; Sequence 2, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529, 279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-529-279-2

Alignment Scores:
Pred. No.: 1,21e-09      Length: 504
Score: 178.00           Matches: 83
Percent Similarity: 40.88%  Conservative: 65
Best Local Similarity: 22.93%  Mismatches: 116
Query Match: 6.95%       Indels: 98
DB: 4                   Gaps: 18

US-09-935-124A-1 (1-1422) x US-09-529-279-2 (1-504)

QY 330 GCAAGAGAAAAAC-----TCCGAGAGAGAGAGATGCGATGAGAGCTTGTG 380
D 3 AlaGlnArgArgSerLeuGlnSerGlnGlnProSerTrpThrAspLeu--- 21
QY 381 GAAAAAGAAAGTTGTAAAGCCTTCCGGTG---ATCTTGTGTGAAGGGCTATGGCT 437
D 22 -----ProLeuCyHisLeuSerGlyValGlySerAlaSerAsnArgSerTyrSerAla 39
QY 438 GAGCGAAAGGAGTGAAGAGGAGAGATGCGATGCCACGTCATCCTGAACGACATCAC 497
D 40 AspGlyLysGly-----Thr 44
QY 498 GAGAGGTGAGGCCCCCATCGCTCCATTT-----ACTCGGGTTTCATAT 542
D 45 GluSerHisProProGlnAspSerTrpLeuLysPheArgSerGlnAsnLysCysPheLeu 64
QY 543 TTTCGTGTTTGTGAGCATGAGAGAAATTCGAGCCTCAAAATTTGCTGCACAGAAATTTG 602
D 65 TyrGlyValPheAsnGlyTyrArgSerGlnAsnArgValThrAsnPheValAlaGlnLysLeu 84

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Db      65 TyrGlyValPheAenGlyTyrAspGlyAsnArgValThrAsnPheValAlaGlnArgLeu 84
QY      603 CATCAAACTTAAATCAGAAAAATTTCTTAAGAGATGAAATCACTGATGAGAAAACCGTG 662
Db      85 SerAlaGlnLeuLeu-----LeuGlyGlnLeuAsnAlaGlnHisAlaGlnAlaAspVal 102
QY      663 AAGAGATGCTTTTGGACACTTTCAGACATCTACTGATGAAAGATTCCTT----- 710
Db      103 ArgArgValLeuLeuGlnAlaPheAspValValGlnArgSerPheLeuGlnSerLeuAsp 122
QY      711 -----AAACAAGCTTCAGCCAGAAAG----- 731
Db      123 AspAlaLeuAlaGlnLysValAsnSerLeuGlnSerGlnLeuProGlnGlyValProGlnHis 142
QY      732 -----CCTGCTCGGAAA----- 743
Db      143 GlnLeuProProGlnTyrGlnLysValLeuGlnLysArgLeuLysThrLeuGlnLysGlnLe 162
QY      744 ---GATGGTCCACTGCGCATGTGTCTGCTGTAGACAAATTTCTTATTTATTTGCGCAAC 800
Db      163 SerGlyGlyAlaMetAlaValAlaValAlaValLeuLeuAsnAlaLeuLysValAlaAsn 182
QY      801 CTCGAGATAGTCGGGCAATCTGTGTGCTTATATGAGGAGAGATCAAAAACATGACAGCC 860
Db      183 ValGlyThrAsnArgAlaLeuLeuLeuCysLysSerThrValAspGlyLeuGln-----Val 200
QY      861 TTAAAGCTTCAGAAAGACATTAATCCAACTCAGTATGAAAGCGGATGAGATACAGAG 920
Db      201 ThrGlnLeuAsnValAspHisThrThrGlnAsnGlnAspGlnLeuPheArgLeuSerGln 220
QY      921 GCTGGA-----GAAAAGTCAGAGATGAGCGGCTTTTGGGCTCTGAGAGTGTCA 971
Db      221 LeuGlyLeuAspAlaGlyLysValLeuGlnValGlyLeuGlyLeuGlnSerThr 240
QY      972 CGCTCCATTGGGACCGGACAGTACAG--CGCTCGGCTGTCACTTGTG----- 1019
Db      241 ArgArgGlyLeuGlyAsp-----TyrLysValLysTyrGlyTyrThrAspAlaAspLeu 258
QY      1020 -----CCGACATCAGACCGCTGCACAGCTGACC 1046
Db      259 SerAlaAlaLysSerLysProLeuLeuAlaGlnProGlnLysGlyAlaGln----- 276
QY      1047 CCCAAATGAC-----AGTTTCATTTTGGCTGAGCTGATGAGGCTCTTCAGAGTCTTT 1097
Db      277 ProLeuAspGlyValThrGlyPheLeuValLeuMetSerGlnGlyLeuTyrLysAlaLeu 296
QY      1098 ACC-----CCAGAGAAGCCGCTGAACCTTCACTTCGCTGCTGAGAGATGAA 1145
Db      297 GlnAlaAlaHisGlyProGlyGlnAlaAsnGlnLysLeuAlaMetLeuAspThrGln 316
QY      1146 AAGATCCAGACCGGGAAGGAGATCCGACAGCCGCGCTACAGAAAGCCCTGCAGAC 1205
Db      317 PheAlaLys-----GlnThrSerLeuAspAlaValAlaGlnAlaValAlaAsp 332
QY      1206 AGGCTG 1211
Db      333 ArgVal 334

RESULT 24
US-09-529-279-43
; Sequence 43, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: OHTOMO, TOSHIIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 051466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PCT FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188

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; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-43

Alignment Scores:
Pred. No.: 1,23e-09 Length: 513
Score: 178.00 Matches: 83
Percent Similarity: 40.88% Conservative: 65
Best Local Similarity: 22.93% Mismatches: 116
Query Match: 6.95% Indels: 98
Gaps: 18
DB: 4

US-09-935-124a-1 (1-1422) x US-09-529-279-43 (1-513)
QY      330 GCMAAGAGAAAACC-----TCCAGAAAGAGAAATGCGAGATGAGAGCTTGTG 380
Db      12 AlaGlnArgArgSerLeuLeuGlnSerGlnGlnGlnProSerThrPheAspLeu----- 30
QY      381 GAAAAGAAAGTTTGTAAAGCTCTTCCGTC--ATCTTGGCTTGAAAGGCTATGCGGCT 437
Db      31 -----ProLeuCysHisLeuSerGlyValGlySerAlaSerAsnArgSerTyrSerAla 48
QY      438 GAGCGAAGAGGTGAGAGGAGAGAGATGACAGATGCCACGTATCTGAAACATCAGAC 497
Db      49 AspGlyLysGly----- 53
QY      498 GAGAGAGTGAAGCCCCCATCTGTCCTCATT-----ACTCGGTTTCATAT 542
Db      54 GlnSerHisProProGlnLysAspSerThrLeuLysPheArgSerGlnAsnLysCysPheLeu 73
QY      543 TTTTCGTTTGGTGAAGCATGAGAGAAATTCAGACCTCAAAATTTGCTGACAGATTTG 602
Db      74 TyrGlyValPheAsnGlyTyrAspGlyAsnArgValThrAsnPheValAlaGlnArgLeu 93
QY      603 CATCAAACTTAAATCAGAAAAATTTCTTAAGAGATGAAATCACTGATGAGAAAACCGTG 662
Db      94 SerAlaGlnLeuLeu-----LeuGlyGlnLeuAsnAlaGlnHisAlaGlnAlaAspVal 111
QY      663 AAGAGATGCTTTTGGACACTTTCAGACATCTACTGATGAAAGATTCCTT----- 710
Db      112 ArgArgValLeuLeuGlnAlaPheAspValValGlnArgSerPheLeuGlnSerLeuAsp 131
QY      711 -----AAACAAGCTTCAGCCAGAAAG----- 731
Db      132 AspAlaLeuAlaGlnLysValAsnSerLeuGlnSerGlnLeuProGlnGlyValProGlnHis 151
QY      732 -----CCTGCTCGGAAA----- 743
Db      152 GlnLeuProProGlnTyrGlnLysValLeuGlnLysArgLeuLysThrLeuGlnLysGlnLe 171
QY      744 ---GATGGTCCACTGCGCATGTGTCTGCTGTAGACAAATTTCTTATTTATTTGCGCAAC 800
Db      172 SerGlyGlyAlaMetAlaValAlaValAlaValLeuLeuAsnAlaLeuLysValAlaAsn 191
QY      801 CTCGAGATAGTCGGGCAATCTGTGTGCTTATATGAGGAGATCAAAAACATGACAGCC 860
Db      192 ValGlyThrAsnArgAlaLeuLeuLeuCysLysSerThrValAspGlyLeuGln-----Val 209
QY      861 TTAAAGCTTCAGAAAGACATTAATCCAACTCAGTATGAAAGCGGATGAGATACAGAG 920
Db      210 ThrGlnLeuAsnValAspHisThrThrGlnAsnGlnAspGlnLeuPheArgLeuSerGln 229
QY      921 GCTGGA-----GAAAAGCTCAGAGATGAGCGGCTTTTGGGCTCTGAGAGTGTCA 971
Db      230 LeuGlyLeuAspAlaGlyLysValLeuGlnValGlyLeuGlyLeuGlnSerThr 249
QY      972 CGCTCCATTGGGACCGGACAGTACAG--CGCTCGGCTGTCACTTGTG----- 1019

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Db 250 ArgAaGIIeGIyAsp-----TyrLysValLysTyrGIyTyrThrAspIleAspLeuLeu 267
Qy 1020 -----CCGACATCAGACGCTGCCAGCTGACC 1046
Db 266 SerAlaAlaLysSerLysProIleIleAlaGluProGluIleHisGIyAlaGln----- 285
Qy 1047 CCCAATGAC-----AGGTTCAATTTGTTGGCTGTGATGGCTCTTCAAGGCTCTT 1097
Db 286 ProLeuAspGIyValThrGIyPheLeuValLeuMetSerGIuGIyLeuTyrLysAlaLeu 305
Qy 1098 ACC-----CCAGAGAGCCGCGTGAATTCATCTTCGCTGCTCCGACGATGAA 1145
Db 306 GluAlaAlaHisGIyProGIyGlnAlaAsnGlnIleIleAlaMetIleAspThrGln 325
Qy 1146 AAGATCCAGACCCGGAGAGGAGTCCGACGCCGCTACAGACAGCTGCAAC 1205
Db 326 PheAlaLys-----GlnThrSerLeuAspAlaValAlaGlnAlaValAla 341
Qy 1206 AGGCTG 1211
Db 342 ArgVal 343

RESULT 25
US-09-529-279-11
; Sequence 11, Application US/09529279
; Patent No. 6451617
; GENERAL INFORMATION:
; APPLICANT: ONO, KOICHIRO
; APPLICANT: ONOMO, TOSHIHIKO
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: METHOD OF SCREENING TGF-BETA INHIBITORY SUBSTANCES
; FILE REFERENCE: 053466/0278
; CURRENT APPLICATION NUMBER: US/09/529,279
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: PCT/JP98/04796
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: JP 9/290188
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-279-11

Alignment Scores:
Pred. No.: 1,236-09 Length: 517
Score: 178.00 Matches: 83
Percent Similarity: 40.88% Conservative: 65
Best Local Similarity: 22.93% Mismatches: 116
Query Match: 6.95% Indels: 98
DB: 4 Gaps: 18

US-09-935-124a-1 (1-1422) x US-09-529-279-11 (1-517)
Qy 330 GCAAGAGAAAAAC-----TCCGAGAGAGAGAAATGACAGTGAAGCTTGTG 380
Db 3 AlAGlnAArgSerLeuLeuGlnSerGIuGlnGlnProSerThrAspLeu----- 21
Qy 381 GAAAAAGAAAGTTTAAAGCCTCTTCGGTG---AATCTTGCTGAAGGCTATGTGGCT 437
Db 22 -----ProLeuCyHisLeuSerGIyValGIySerAlaSerAsnArgSerTyrSerAla 39
Qy 438 GAGCGGAAGGCGAGAGGAGGAGATGCAGATGCCACGTCATCTCTGAACATCAACC 497
Db 40 AspGIyLysGIy-----Thr 44
Qy 498 GAGAGTGAAGCCCCCATCGTCCCTCATTT-----ACTCGGCTTTCATAT 542
Db 45 GluSerHisLeuProGIyAspSerTyrLeuLysPheArgSerGIuAsnAsnCySerPheLeu 64
Qy 543 TTTGCTGTTTGTATGACATGAGAAATTCAGAGCTCAAAATTGCTTCAGAAATTTG 602

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Db 65 TyrGIyValPheAsnGIyTyrAspGIyAsnArgValThrAsnPheValAlaGlnArgLeu 84
Qy 603 CATCAAACTTAATCAGAAAAATTTCTTAAGGAGATGTAAATCAGTGTGAGAAAAACCGG 662
Db 85 SerAlaGluLeu-----LeuGIyGlnLeuAsnAlaGluHisAlaGluAlaAspVal 102
Qy 663 AAGAGATGCTTTTGAACATTTCAAGCATACGTATGAAAGATTCCTT----- 710
Db 103 ArgAaGValLeuLeuGlnAlaPheAspValValGIuArgSerPheLeuGluSerIleAsp 122
Qy 711 -----AAACAAGCTTCCAGCCAGAG----- 731
Db 123 AspAlaLeuAlaGluLysAlaSerLeuGlnSerGIuLeuProGIuGIyValProGlnHis 142
Qy 732 -----CCTGCCTGGAAA----- 743
Db 143 GlnLeuProProGIuThrGIyGlnLysIleLeuGluArgLeuLysThrLeuGluArgGluIle 162
Qy 744 --GATGGATCCATGCGCACCGTGTCTGCTGCTGATGACAACATTTTAAATATGCCAAC 800
Db 163 SerGIyGIyAlaMetAlaValAlaValaLeuLeuAsnAsnLysLeuTyrValAlaAsn 182
Qy 801 CTCGAGATAGTCGGGCAATCTTGTGCTTAAATGAGAGATCAAAAAACATGCAACC 860
Db 183 ValGIyThrAsnArgAlaLeuLeuCyLysSerThrValAspGIyLeuGln-----Val 200
Qy 861 TTAACCTTCAGCAAGACATATCAACTCAGTATGAAAGCGGATGAGATGACAAAG 920
Db 201 ThrGlnLeuAsnValAspHisThrThrGlnLysGlnAspGIyLeuPheArgLeuSerGln 220
Qy 921 GCTGA-----GAAACGTCAGGAGATGGCGCTGTTTGGCGCTGTAAGGTGTCA 971
Db 221 LeuGIyLeuAspAlaGIyLysIleLeuGlnValGIyIleLeuCyGIyGlnLysSerThr 240
Qy 972 CGCTCATTTGGGAGCGGACAGTACAG--CGCTCGGTGTCACCTCTGTG----- 1019
Db 241 ArgAaGIleGIyAsp-----TyrLysValLysTyrGIyTyrThrAspIleAspLeuLeu 258
Qy 1020 -----CCGACATCAGACGCTGCCAGCTGACC 1046
Db 259 SerAlaAlaLysSerLysProIleIleAlaGluProGluIleHisGIyAlaGln----- 276
Qy 1047 CCCAATGAC-----AGGTTCAATTTGTTGGCTGTGATGGCTCTTCAAGGCTCTT 1097
Db 277 ProLeuAspGIyValThrGIyPheLeuValLeuMetSerGIuGIyLeuTyrLysAlaLeu 296
Qy 1098 ACC-----CCAGAGAGCCGCGTGAATTCATCTTGTCTGCTGTGAGATGAA 1145
Db 297 GluAlaAlaHisGIyProGIyGlnAlaAsnGlnIleIleAlaMetIleAspThrGln 316
Qy 1146 AAGATCCAGACCCGGAGAGGAGGAGTCCGACGCCGCTACAGACAGCTGCAAC 1205
Db 317 PheAlaLys-----GlnThrSerLeuAspAlaValAlaGlnAlaValAlaAsp 332
Qy 1206 AGGCTG 1211
Db 333 ArgVal 334

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Search completed: February 9, 2003, 17:55:27
Job time : 39.5 secs